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              The present invention relates to motoneuronotrophic factor peptide analogue, where the peptide analogue enhances the viability of motor neurons. The methods and compositions of the present invention are useful for promoting motor neuron viability and axon degeneration, target muscle reinnervation, treating peripheral nerve injuries, treating neurodegenerative disease and in wound healing. The present sequence represents a MNTF motoneuronotrophic factor peptide analogue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuropeptide-Agonist;
peripheral nerve; neur
                               ADQ90200 standard;
                                                                                                                                                                                                                                                                                                                        New motoneuronotrophic factor peptide analogue enhancing the viability of motor neurons, useful for target muscle reinnervation, treating peripheral nerve injuries or neurodegenerative diseases and in wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
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Neuropeptide-Agonist; axon degeneration; muscle reinnervation;
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mer motoneuronotrophic factor peptide analogue

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neurons. T
for promot
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21-JAN-2003;
                                                     21-JAN-2004; 2004WO-US001468.
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                                                                                                                                                                                                                 Unidentified
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reinnervation, treating peripheral nerve injuries, treating
neurodegenerative disease and in wound healing. The present sequence
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2003US-0441772P
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                                                 The invention relates to an isolated polynucleotide consisting of motoneuronotropic factor (MNTF)-associated nucleic acid sequence comprising AEA17647 or AEA17648, its fragment or complement. Also
                                                                                                                                                                                                                New isolated polynucleotide consisting of a motoneuronotropic factor (MNTF)-associated nucleic acid sequence, useful for promoting the survival, growth, proliferation and maintenance of mammalian neurons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MNTF; cell growth; cell proliferation;
16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ances the viability of motor the present invention are useful axon degeneration, target muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     œ
•••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            method for determining the presence of a MNTF-associated polynucleotide in a medium, a method of comparing the relative abundance of MNTF associated expression products in different samples; and a panel for use in hybridization assay comprising two or more polynucleotides stably associated with the surface of a solid support. The polynucleotides are useful for promoting the survival, growth, proliferation and maintenance of mammalian neurons. The present sequence represents a polypeptide encoded by an open reading frame of MNTF CDNA (see AEA17647), which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    frame of SEQ ID No. 1; a fusion protein comprising an MNTF associated polypeptide encoded by an open reading frame of SEQ ID no. 1 linked to heterologous protein; an expression vector operably linked to the isolated polynucleotide, where at least one open reading frame is operably linked to a control sequence compatible with a desired host vector; an isolated host cell transformed with the expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Motorneuronotrophic factor; MNTF-1; MNTF1-F6; human; axon regeneration; motoneuron; diagnose; treatment; disease; wound healing; scar tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human MNTF1-F6
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                                         This sequence, represents a fragment of a novel human motoneurotrophic factor, MNTF1-F6. Such factors are used to promote regeneration of the axon of a motoneurone, to diagnose and treat motoneurone disease in a mammal or to accelerate wound healing whilst concomitantly minimising inhibiting scar tissue and/or keloid formation in an area associated wound healing whilst concomitantly minimising inhibiting scar tissue and/or keloid formation in an area associated wound healing whilst concomitantly minimising in a second second with the second s
                                                                                                                                                                                                                                                                                                                                                                                        Motoneurotrophic factor MNTF1-F3 and MNTF1-F6 - regeneration, diagnosing or treating motoneuron wound healing without scar formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-1996;
15-NOV-1996;
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a wound. For promoting axonal regeneration, the
                                                                                                                                                                                                                                                                                                              Claim 4; Fig 2B; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-230703/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KMBI-) KM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 located
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
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96US-00751225.
97US-00928862.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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polypeptide
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                             The invention relates to a method for promoting the survival, growth, proliferation or maintenance of mammalian neurons by administering motoneuronotrophic factors (MNTF). The method is useful for treating peripheral nerve injuries, musculoskeletal disorders, spinal cord injuries, head injuries, strokes, neuromuscular degenerative diseases, amyotrophic lateral sclerosis, spinal muscular atrophy, peripheral neuropathy, diabetic peripheral neuropathy, peripheral neuropathy resulting from AIDS or radiation therapy for cancer, multiple sclerosis, muscular dystrophy, inhibition of scar formation, myasthenia gravis and sensory neuronal function disorders. The present sequence is human MNTF1-F6 protein used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peripheral nerve injury; musculoskeletal disorder; spinal cord injury; head injury; stroke; neuromuscular degenerative disease; nootropic; amyotrophic lateral sclerosis; peripheral neuropathy; neuroprotective; muscular dystrophy; AIDS; spinal muscular atrophy; multiple sclerosis; sensory neuronal function disorder; vulnerary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAO29914 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           administered at a concentration of 5 ng-50 mg, whereas for inhibiting hereditary motoneurone disease, the dosage is 5-100 (especially 30-50)ng
                                                                                                                                                                                                                                              Promoting the survival, growth, proliferation or maintenance of neurons by administering motoneuronotrophic factors, useful for musculoskeletal and neurodegenerative disorders and spinal cord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human motoneuronotrophic factor (MNTF)1-F6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-SEP-2003
                                                                                                                                                                                                                                                                                                                 N-PSDB;
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                                                                                                                                                                                                                   Claim 1; Fig 2B;
                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2001; 2001US-00989481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       motoneuronotrophic factor; MNTF; therapy; radiation therapy; earal nerve injury; musculoskeletal disorder; spinal cord injury;
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                                                  gravis and
human MNTF1-
                                                                                                                                                                                                                                                 mammalian
r treating
l injuries.
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Query Match Best Local Matches

h 100.0%; Similarity 100.0%; 6; Conservative 0

0;

Score 31; Pred. No.

DB 6

Length 33;

red. No. 11; Mismatches

0

Indels

0

Gaps

0

Sequence

33

ΑA,

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ADQ90159
ADQ
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AAUS7756
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  XXXXXXXXX
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to motoneuronotrophic factor peptide analogue, where the peptide analogue enhances the viability of motor neurons. The methods and compositions of the present invention are useful for promoting motor neuron viability and axon degeneration, target muscle reinnervation, treating peripheral nerve injuries, treating neurodegenerative disease and in wound healing. The present sequence represents MNTF1-F6 33 mer motoneuronotrophic factor peptide analogue.
  SAPHO syndrome;
                                               Propionibacterium acnes immunogenic protein #18652.
                                                                                                           27-FEB-2002
                                                                                                                                                                                                              AAU57756 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; SEQ ID NO 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New motoneuronotrophic factor peptide analogue enhancing the viability of motor neurons, useful for target muscle reinnervation, treating peripheral nerve injuries or neurodegenerative diseases and in wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-562147/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2003; 2003US-0441772P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004065410-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peripheral nerve;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  motoneuronotrophic; motor neuron; Nootropic; Neuroprotective; Vulnerary;
Neuropeptide-Agonist; axon degeneration; muscle reinnervation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNTF1-F6 33 mer motoneuronotrophic factor peptide analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-OCT-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33
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                                                                                                        (first
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synovitis;
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                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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  acne;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
pustulosis; hypertosis; osteomyelitis;
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RESULT 11
ABM54275
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XXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in CC the treatment, prevention and diagnosis of medical conditions caused by A acnes. The disorders include SAPHO syndrome (synovitis, acne, CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. CC P. acnes is also involved in infections of bone, joints and the central CC nervous system, however it is particularly involved in the inflammatory CC lesions associated with acne vulgaris. A method for detecting the CC presence or absence of P. acnes in a patient comprises contacting a CC sample with a binding agent that binds to the proteins of the invention CC and determining the amount of bound protein in the sample. The CC specific for P. acnes proteins. These antibodies can be used to CC downregulate expression and activity of P. acnes proteins determining P. acnes proteins may also be used as CC diagnostic agents for determining P. acnes presence, for example, by CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was CC obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                          Query Match
Best Local
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02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris.
                           Propionibacterium acnes predicted ORF-encoded polypeptide #18951.
                                                              20-OCT-2003
                                                                                                                           ABM54275 standard; protein; 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 18951; 1069pp; English
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                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
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                                                                                                                                                                                                            14 FSRYAR 19
                                                                                                                                                                                                                                         1 FSRYAR 6
                                                                                                                                                                                                                                                                        l Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                          81
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/e J, Zhang
                                                                                                                                                                                                                                                                           Conservative
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2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0199047P
                                                           (first entry)
                                                                                                                                                                                                                                                                                          100.0%;
100.0%;
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                                                                                                                                                                                                                                                                           <u>.</u>
                                                                                                                                                                                                                                                                                          Score 31; DE
Pred. No. 28;
                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                          DB
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                                                                                                                                                                                                                                                                                                          Length 81;
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                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunogenic are used in
                                                                                                                                                                                                                                                                           Gaps
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Acne vulgaris;

antiseborrhoeic;

dermatological; antibacterial;

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RESULT 12
AAU57258
ID AAU57
XX
AC AAU57
XX
AC AAU57
XX
DT 27-FE
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                                                                                                                                                                                                                                                                                                                                                                                   CC encoding a Propionibacterium acnes protein. The invention also relates to CC polypeptides encoded by the polynucleotides (ABM35624-ABM6436) and to cadditionally encompasses expression vectors and host cells comprising a polypeptides. The invention CC additionally encompasses expression vectors and host cells comprising a copynucleotide of the invention; antibodies against polypeptides of the invention; a comprising a polypeptide of the invention; a comprising a polypeptide of the invention; a comprising a polypeptide of the invention; a comprising polypeptide of the invention; a come to the invention; a comprising polypeptides of the invention; a comprising polypeptides of the invention; a come to the invention; a comprising polypeptides; a method for a polypeptides, comprising polypeptides, comprising polypeptides, compared comprising polypeptides, composition (comprising polypeptides, compared composition (comprising polypeptides, compared composition); a method and kit for detecting or determining the presence or absence of p. acnes in a comparison. The p. acnes polypeptides, polypucleotides, antibodies, fusion proteins, determining the development of p. acnes in a comparison. The p. acnes polypucleotides, polypucleotides, antibodies, fusion proteins, determining an immune response specific for a p. acnes composition. The polymucleotides can also be used as probes or primers for concleic acid hybridisation. The vaccine composition is useful for the comparison of an immune response specific for a p. acnes composition is useful for the comparison of an immune response specific for a p. acnes comparison. The present composition is useful for the comparison of a c
                                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitcham JL, Skeiky YAW, Pers
Zhang Y, Wang S, Jen S, Lod
Barth B, Vallieve-Douglass J;
                                         AAU57258;
                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 18951; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-381789/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-OCT-2001; 2001US-00978825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2002; 2002WO-US032727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Propionibacterium acnes
  27-FEB-2002
                                                                                   AAU57258 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunostimulant; immune response; vaccine.
                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                              1 FSRYAR 6
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                                                                                                                                                                                         FSRYAR 19
                                                                                                                                                                                                                                                                                                                                                         81
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A
                                                                                                                                                                                                                                                                          Conservative
  (first entry)
                                                                                                                                                                                                                                                                                         100.0%; Score 31; DB 6; Length 81; 100.0%; Pred. No. 28;
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Lodes MJ,
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                                                                                                                                                                                                                                                                          Mismatches
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Benson DR,
                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                          Indels
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  RESULT 13
ABM53777
ID ABM53
XX
AC ABM53
XX
AC ABM53
XX
DT 20-00
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    20-OCT-2003
                                             ABM53777;
                                                                                   ABM53777
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S

standard; protein; 112

(first entry)

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Matches
                                                                                                                                                         Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                               nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (BLISA). Note: The sequence data for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
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02-JUN-2000; 2000US-0208841P
07-JUL-2000; 2000US-0216747P
                                                                                                                                                                                                                                                         Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                   this patent did not form part of the printed specification, obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the treatment, prevention and diagnosis of medical conditions caused by p. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteowyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 18453; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L'maisonneuve
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                                                                                                                           Local Similarity
nes 6; Conserv
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FSRYAR
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                                                                                                                                                         100.0%; Score 31; 100.0%; Pred. No.
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                                                                                                                                 Mismatches
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                                                                                                     Matches
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Zhang Y,
Barth B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an invention also relates tencoding a Propionibacterium acnes protein. The invention also relates tencoding a Propionibacterium acnes protein. The invention and to polypeptides encoded by the polypuncleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                        Sequence 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID NO 18453; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-2001; 2001US-00978825
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                                                                                                                                                                                                                                                     invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format direct from WIPO at ftp.wipo.int/pub/published pct sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-)
                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to an isolated polynucleotide (ACF64435-ACF64733) oding a Propionibacterium acnes protein. The invention also relates to
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FSRYAR
                                                  FSRYAR 6
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Vallieve-Douglass
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ng S, Jen S,
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Lodes MJ,
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Pred. No. 39;
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Benson DR,
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Jones R, Carter
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ABM64633 ID ABM6

ABM64633 standard; protein;

174 AA

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35 FSRYAR 1 FSRYAR 6 Similarity 6; Conser

Query Match Best Local S Matches 6

Conservative

<u>,</u>

100.0%;

Score 31; DB Pred. No. 61; Mismatches

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Length 174; Indels

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cc encoding a Propionibacterium acres protein. The invention also relates to complypeptides encoded by the polynucleotides (ABM3524-ABM6435) and to complypeptides encoded by the polynucleotides. The invention additionally encompasses expression vectors and host cells comprising a polypeptide of the invention; an immuner response specific for a p. acres or invention; a this method; a vaccine composition proteins, or comprising a polypeptide of the invention; a compression proteins comprising a polypeptide of the invention; a complete the invention; a complete the invention; a composition comprising p. acres polypeptides, antibodies, antibodies, fusion proteins, T cell populations, or comparising p. acres polypeptides, composition (comprising p. acres polypeptides, comparising p. acres in a comparisint; and a method for inhibiting the development of p. acres in a composition; and a method for inhibiting the development of p. acres in a composition. The p. acres polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the collypeptides are useful for diagnosing, preventing or treating acres consistent. The polynucleotides can also be used as probes or primers for configuration of an immune response against p. acres in p. acres in a composition of an immune response against p. acres or primers for composition of an immune response against p. acres, or for treating acre, can determine the development of p. acres in a consequence represents a specifically claimed p. acres or primers for the printed specification, but was contained in electronic format directly from WIPO at the printed specification, but was contained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang Y,
Barth B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; SEQ ID NO 29309; 1481pp; English.
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174 AA;
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Lodes MJ,
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Benson DR,
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Jones R, Carter
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Best Local Similarity
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Chlamydial infection; antigen; immunogen; vaccine; diagnosis; human respiratory disease; cardiovascular disease; atherosclerosis; coronary artery disease; carotid artery stenosis; myocardial infarction;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Griffais R;
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13-SEP-1999
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29-JUL-2002
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                                                                                                                         pneumoniae cp7224 protein, SEQ ID NO:107
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RESULT 17
ABU27032
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                                                                                                                                                                                                                                                                                                                                       CC Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia CC pneumoniae (etrain CWLO29), and ABL91184-ABL91373 represent DNA encoding Ct them. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia CC pneumoniae is a common cause of respiratory disease in humans, and is CC also involved in the development of cardiovascular diseases such as CC atherosclerosis, coronary artery disease, carotid artery stenosis, CC myocardial infarction, cerebrovascular disease, aortic aneurysm, CC claudication and stroke. The proteins and nucleic acids of the invention CC may be used in vaccines and pharmaceutical compositions for the prevention or treatment of chlamydial infections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of CC chlamydia pneumoniae, and the nucleic acids may be used in pCR, branched CC pneumoniae gene expression. The present sequence represents a cCC (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                  Query Match
Best Local (
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11-JUL-2000; 2000GB-00017947.
21-JUL-2000; 2000GB-00017983.
07-AUG-2000; 2000GB-00019368.
18-AUG-2000; 2000GB-00020440.
14-SEP-2000; 2000GB-00022543.
10-NOV-2000; 2000GB-00027549.
22-DEC-2000; 2000GB-00031706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUL-2000;
11-JUL-2000;
21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamyc preferably Chlamydia pneumoniae, and for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cerebrovascular disease; aortic aneurysm; claudication; stroke;
strain CWL029.
            Protein encoded by Prokaryotic
                                          23-OCT-2003
19-JUN-2003
                                                                                        ABU27032;
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-2001; 2001WO-IB001445
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                                                                                                                  ABU27032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 93; 364pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABL91237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JAN-2002
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                                                                                                                                                                                           135
                                                                                                                                                                                                                                                  l Similarity
6; Conserv
                                                                                                                                                                                                                 FSRYAR 6
                                                                                                                    standard;
                                                                                                                                                                                           FSRYAR 140
                                                                                                                                                                                                                                                                                                                357 AA;
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                                                                                                                                                                                                                                                     Conservative
                                          (revised)
(first entry)
                                                                                                                  protein;
                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                    357
                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                Score 31; DB 5;
Pred. No. 1.3e+02;
              essential
                                                                                                                                                                                                                                                     Mismatches
              gene
                                                                                                                                                                                                                                                                                Length 357;
                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                     Gaps
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Antisense; prokaryotic essential gene; cell proliferation; drug design.

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                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding a polypeptide whose expression is inhibited by the antisense controlled acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for consider the gene product or that has an activity against a biological pathway of the gene product or that has an activity against a biological pathway of centifying a gene required for cellular proliferation or the biological pathway of identifying a gene required for cellular proliferation or the biological pathway or a gene on which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent convenient of the strains; or (13) identifying the target of a compound that inhibits the gene proliferation of an organism. The antisense nucleic acids are useful for identifying the target of a compound that inhibits the gene proliferation of an organism. The antisense nucleic acids are useful for identifying the target of a compound that inhibits the gene proliferation of an organism. The antisense nucleic acids are useful for identifying the target of a compound that inhibits the gene proliferation of an organism. The antisense nucleic acids are useful for identifying the carget of a compound that inhibits the gene proliferation of an organism. The antisense nucleic acids are useful for identified acids are useful for identified acids are useful for identified acids.
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Wall
                                                                                                                                                                                                                                                                 identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2001;
08-FEB-2002;
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                                                                                                                                                                            Sequence
                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences. (Updated on
standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e 6213 antisense sequences given in the specification where expression the nucleic acid inhibits proliferation of a cell. Also included are:
) a vector comprising a promoter operably linked to the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ָט נָי
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                                                                                                              Similarity
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Trawick
                                               FSRYAR 6
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; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
                                                                                       Conservative
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Carr GJ,
                                                                                                          100.0%; Score 31; DB 6;
100.0%; Pred. No. 1.3e+02;
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                                                                                    Mismatches
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Yamamoto R,
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Forsyth
                                                                                                                               Length 357;
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Xu HH;
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RESULT 19 ADS44828

ADS44828

ADS44828 standard; protein; 463

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RESULT 18
AEC95703
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                                                                                                                                                                                                                                                         The invention relates to a polypeptide for use as an autotransporter cantigen. Also provided is a method of eliciting an immune response in an individual which involves administering to the individual an Chlamydia pneumoniae autotransporter protein selected from Cpn0794, Cpn0795. Cpn0795, or Cpn0799 or an immunogenic fragment. The polypeptide is secreted into the cytoplasm of the host cell through a Crype v autotransporter secretion system mechanism. The polypeptide is useful as an antigen for raising a C. pneumoniae specific immune response in an cresponse. It is also useful for raising a systemic immune response in an Crype valual infected with C. pneumoniae. The polypeptide is diagnosis. It can also be used in the preparation of a medicament for the prevention or treatment of a C. pneumoniae infection in an individual. It can also be used as an autotransporter confection which immunoreacts with seropositive serum of an individual infected with C. pneumoniae. The preparation of an individual in the preparation of an individual in the preparation of an autotransporter confection which immunoreacts with seropositive serum of an individual in the preparation of an autotransporter content which content is the preparation of an individual in the preparation of an autotransporter content in the preparation of an individual in the preparation of an individual in the preparation of an autotransporter content in the p
                                                                                              Matches
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12-JAN-2005; 2005US-0643110P
19-JAN-2005; 2005US-0644552P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEC95703 standard; protein; 357 AA.
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis; autotransporter antigen; antibacterial; vaccine;
MurG peptidoglycan transferase protein; CPn 0904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-2005
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                                                                                                                                                                                                                                          pneumoniae MurG peptidoglycan transferase protein (CPn 0904)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autotransporter antigen, for raising a specific immune respons
preventing or treating C. pneumoniae infections in individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Chlamydia pneumoniae autotransporter protein, useful as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENBANK; AAD19042.1.
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135 FSRYAR 140
                                             1 FSRYAR 6
                                                                                           h 100.0%;
Similarity 100.0%;
6; Conservative 0
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                                                                                                                     Score 31;
Pred. No.
                                                                                                   Mismatches
                                                                                                                       1.3e+02;
                                                                                                                                              DB 9;
                                                                                                                                              Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune response
                                                                                                   Indels
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                                                                                                                                                    CC having an improved property comprises transforming a plant with the CC recombinant DNA construct and growing the transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant properties. CC The recombinant DNA construct is useful for producing plant properties. CC improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of CC homologous recombination, modified seed oil or protein yield and/or CC content, improved yield by modification of carbohydrate, nitrogen or CC content, improved plant growth and development under at least one stress croduction. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not CC form part of the printed specification but was obtained in electronic CC format from USPTO at sequence.html.
                                                                Matches
                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                               microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     provide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 23258; 122pp; English.
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                                                                                                                               Sequence 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HINK/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates
76
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SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                r functional in a plant cell, where the promoter is positioned to for expression of a polynucleotide encoding a polypeptide from a
                                                              Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHEN X.
GOLDMAN B S.
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FSRYAR
                               FSRYAR 6
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                                                                Conservative
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81
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                                                                              100.0%;
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                                                                              Score 31; DB 8;
Pred. No. 1.7e+02;
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                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      construct comprising
                                                                                              Length 463;
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AABZULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for excluding homology between two protein families. The method involves constructing models for secondary structural elements for each family, aligning secondary structural elements for each family structural elements from the
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homologous recombination; seed oil yield; protein yield; carbohydrate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADS45088 standard; protein; 474 AA
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                               21-FEB-2002; 2002US-0360039F
                                                                                 20-FEB-2003; 2003US-00369493
                                                                                                                                        18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity hes 6; Conserv
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DB; AAS52536.
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                                                                                                                                                                                                                                                                                                     polypeptide
                                                                                                                                                                                                                                                                                                                            phosphorus; photosynthesis; lignin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 31; DB 4; I ilarity 100.0%; Pred. No. 1.7e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
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Xu HH;
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RESULT 23
ABO74595
ID ABO74
XX
XX
ABO74
XX
AC ABO74
DT 29-JU
DX
DE Pseud
XX
Bacte
XX
Bacte
XX
US655
XX
US655
XX
PS 18-FI
XX
18-FI

Bacterial infection;

Pseudomonas

aeruginosa infection;

antibacterial

Pseudomonas aeruginosa

US6551795-B1

18-FEB-1998; 18-FEB-1999;

98US-0074788P 99US-00252991 Pseudomonas aeruginosa polypeptide #6770.

29-JUL-2004

(first entry)

ABO74595 standard; protein; 509

밁 S

157 FSRYAR 162

1 FSRYAR

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Conservative

0

Mismatches

Indels

0

Gaps

0

.7e+02;

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Query Match
Best Local Similarity
""" hes 6; Conserv?
                                                                                                             comprising the recombinant DNA construct and a method of producing a crop plant of transformed plant having an improved property. The plant is a crop plant comprising the recombinant DNA construct and a method of producing a crop plant comprise or soybean. The method of producing a transformed plant component plant comprises transformed plant with the crop plant comprises transformed plant with the crop plant properties and growing the transformed plant with the component plant properties the transformed plant with the component plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plant properties. Increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of the cell cycle pathway with plant growth regulators, increased rate of the component properties and/or uptake, by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth as bacterial polypeptide used in the growth form part of the printed specification but was obtained in electronic form part for the grinted specification but was obtained in electronic confirmance html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant DNA construct comprising a promoter positioned to provi
for expression of a polynucleotide encoding a polypeptide from a
microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CAOY/)
(HINK/)
(SLAT/)
(CHEN/)
(GOLD/)
                                                                                                           Sequence 474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promoter functional in a plant cell, where the promoter is positioned provide for expression of a polynucleotide encoding a polyneptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-061375/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a recombinant DNA construct comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 23518; 122pp; English.
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SLATER S
CHEN X.
GOLDMAN
                                                                                                                                                     from USPTO
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                                            100.0%; Score 31; 100.0%; Pred. No. 1
                                                                                                                                                     seqdata.uspto.gov/sequence.html.
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                                                                     DB 8;
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                                                                Length 474
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RESULT 24
ABG24444
ID ABG24
XX ABG24
XX ABG24
XX INOVel
DT 18-FF
XX Human
KW Human
KW Food
XX Homo
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a
N-PSDB;
                                                                                        Drmanac
                                                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                          11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #24435
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                                                                                                                                                (HYSE-) HYSEQ INC.
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                              2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n; chromosome mapping; gene mapping; gene therapy; forensic;
supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003-615309/58
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                                                                                     RT,
   AAS88631
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                                                                                     Liu C,
                                                                                                                                                                                                          2000US-00540217.
2000US-00649167.
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                                                                                     Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 7;
Pred. No. 1.8e+02;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The
                                                                         involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 54803; 103pp; English
                                                    ftp.wipo.int/pub/published
                                                    _pct_sequences
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멁 5 Matches Query Match Best Local 613 FSRYAR 618 l Similarity 6; Conserva 1 FSRYAR 6 Conservative 100.0%; 0 Score 31; DB 4; Pred. No. 4.5e+02; Mismatches 0, Length 1225; Indels 0 Gaps 0

Sequence 1225

AΑ;

RESULT 25 ABG24819 ID ABG24 Novel human diagnostic protein #24810 ABG24819 standard; protein; 1258 AA 18-FEB-2002 (first entry)

supplement; chromosome mapping;
upplement; medical ir imaging; gene mapping; gene therapy; forensic
maging; diagnostic; genetic disorder.

Homo sapiens

WO200175067-A2

31-MAR-2000; 23-AUG-2000; 2000US-00649167 2000US-00540217

30-MAR-2001; 2001WO-US008631

HYSEQ INC.

RT, Liu C, Y

WPI; 2001-639362/73

N-PSDB; AAS89006.

New isolated polynucleotide and encoded polypeptides, useful in

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RESULT 26
AAU60688
ID AAU60688
AC AAU60
XX 27-FE
XX SAPHC
KW SAPHC
KW LIVELT
KW INFI
KW OCCUP
PN WO200
XX 01-NC
PD 01-NC
PF 20-AF
XX 21-AF
PR 02-U
PR 07-U
PR 07-U
PR 07-U
PR 07-U
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                   SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveittis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reaction (PCR) primers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostics, for responsible for
WPI; 2001-616774/71.
N-PSDB; AAS59612.
                                                                                                                                                           21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU60688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU60688 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1258 AA;
                                                               L'maisonneuve
                                                                                                                                                                                                                                       20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                                                                                         WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                               Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in diagnostics as expressed sequence tags for identifying expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to isolated polynucleotide (I) and polypeptide (II) uences. (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ortion (PCR) primers, oligomers, and for chromosome and gene אינוען primers, oligomers, and for chromosome and gene שונען, in recombinant production of (II). The polynuclectices are also used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۲
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                                                                                                                        CORIXA CORP
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                                                                                Persing
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                                                                                                                                                                                                                                                                                                                                                                 acnes.
                                                             Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55178; 103pp; English.
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                                                               Mitcham JL, Wang SS,
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58
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Pred. No. 4.6e+02;
; Mismatches 0;
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Mitcham Cahang Y,
Barth B,

JL, Skeiky YAW, Pers , Wang S, Jen S, Lod , Vallieve-Douglass J;

Persing DH, Lodes MJ,

Bhatia Benson [

DR,

Maisonneuve JL; Jones R, Carter

(CORI-)

CORIXA CORP

15-OCT-2001; 2001US-00978825 11-OCT-2002; 2002WO-US032727 24-APR-2003

N-PSDB;

ACF64541.

WPI; 2003-381789/36

New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the treatment, prevention and diagnosis of medical conditions caused by CP acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. CP acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory CP lesions associated with acnes vulgaris. A method for detecting the CP resence or absence of P. acnes in a patient comprises contacting a condition of any condition of the invention and determining the amount of bound protein in the sample. The CP collection of antibodies and determining the amount of bound protein in the sample. The CP collectific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and CP chief of the acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by contact at a contact at the contact and the contact as a contact and the contact as a contact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            this patent did not form part of the printed specification, obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM57207 standard; protein; 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes predicted ORF-encoded polypeptide #21883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABM57207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .mmunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSRYAR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    response; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 58;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
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                                                                                                                   01-AUG-1997;
                                                                                                                                                                                 31-JUL-1998;
                                                                                                                                                                                                                                                                                                              WO9906554-A2
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                           (GEST ) GENSET
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC human secreted proteins, and encode the proteins given in AAY01026 to AAY12260, respectively. The proteins given in AAY01026 the proteins given in AAY010260 and CC AAY11994 to AAY12260, respectively. The proteins given represent the CC signal peptide and an N-terminal fragment of a secreted protein. The CC nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell cyroliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, namentopoiesis regulating cregulating activity, receptor/ligand activity, anti-inflammatory cativity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide into a cell
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                                       Allen SM,
Jones TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acids encoding human secreted proteins - obtained from cDNA libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle and heart tissue.
                                                                                                                                                                                                                                            Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 85
                                                                                  (DUPO )
                                                                                                                                                                                     09-JAN-2003
                                                                                                                                                                                                                                                                        transgenic plant
                                                                                                                                                                                                                                                                                    CKC-like transcription factor; antisense inhibition; co-suppression;
                                                                                                                                                                                                                                                                                                   Plant; oil trait; oil phenotype; altered lipid profile; MAP ) receptor-like protein kinase; mitogen activated protein kinase; LIP15-like transcription factor caleosin; ATP citrate lyase;
                                                                                                                                                                                                                                                                                                                                                              Oryza sativa
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                                                                                                                           29-JUN-2001; 2001US-0301913P
                                                                                                                                                         27-JUN-2002; 2002WO-US020152
                                                                                                                                                                                                                 WO2003002751-A2
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                         Allen V
Kinney
MC;
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                               י WB,
א AJ,
                                                                                                NEMOURS &
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                                        Cahoon
Klein
                                                                                  INT INC
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Pred. No. 1.4e+02;
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                                       Epelbaum S, Fan
Li C, Oliveira
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                                        Famodu OO, H
ira IC, Sakai
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                                                                                                                                                                                                                                                                                                                                 MAP kinase;
                                                       Harvell LT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                        Ή,
                                                                                                                                                                                                                                                                                                        SNF1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                          Shen B;
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N-PSDB; ACC00714.

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RESULT 30
ABR40677
ID ABR40677
AC ABR40
XX ABR40
AC ABR40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an isolated nucleotide fragment (I) C comprising a nucleic acid sequence (NS) chosen from a NS encoding a CC polypeptide (PP) having receptor-like protein kinase activity, mitogen CC activated protein (MAP)-kinase activity, LIPIS-like transcription factor activity and CKC-like transcription factor activity. Also described: (I) CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or CC (III), operably linked to a regulatory sequence; (3) a plant (IV) CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5) CC comprising time of the pression in a transformed plant. (III) is useful for CC constant time or co-suppression in a transformed plant. (III) is useful for CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for CC creating transgenic plants having altered lipid profiles. (I) can also be CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa oil trait related protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 215;
                                                                                                                Allen SM, Allen WB,
Jones TJ, Kinney AJ,
Tarczynski MC;
                                                                                                                                                                                                                                                                                                                     29-JUN-2001; 2001US-0301913P
                                                                                                                                                                                                                                                                                                                                                                            27-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase; receptor-like protein kinase; mitogen activated protein kinase; oil; IIP15-like transcription factor caleosin; ATP citrate lyase; SNF1; CKC-like transcription factor; antisense inhibition; co-suppression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABR40677 standard; protein; 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 90
                                 2003-201509/19
DB; ACC00712.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 5; Conserv
                                                                                                                                                                                                                                   DU PONT DE NEMOURS & CO
PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSKYAR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                               2002WO-US020152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             542pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.3%;
                                                                                                                                              Cahoon
Klein
                                                                                                                                                                                                                                INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB 6; Le
Pred. No. 1.5e+02;
1; Mismatches 0;
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R
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                                                                                                                                              Epelbaum S, Fan
Li C, Oliveira
                                                                                                                                                                                                                                                                 H
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                                                                                                                                           Famodu OO, Harvell LT;
ira IC, Sakai H, Shen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO:174.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    011;
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                                                                                                                                                 B
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21-MAR-1997; 21-MAR-1997; 21-MAR-1997; 21-MAR-1997; 30-MAY-1997; 30-MAY-1997; 30-MAY-1997;

97US-0041276P. 97US-0041281P. 97US-0041281P. 97US-0042344P. 97US-0048069P. 97US-0048094P.

01-OCT-1998

Misc-difference

Location/Qualifiers /label= unknown

sapiens

19-MAR-1998;

98WO-US005311

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RESULT 31
AAW67901
ID AAW67
XX
AC AAW67
AC AAW67
AX
DT 25-M
XX
DT 25-M
XX
Huma
XX
Huma
KW Huma
KW daw
KW daw
KW cog
KW co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder: echipochrenia: recorrect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering phenotypes in plants such as sunflower, coconut, soybean, wheat and i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW67901 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an isolated nucleotide fragment comprising a nucleic acid sequence (NS) chosen from a NS encodir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phenotypes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein encoded by gene 36 clone HODCL36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FSRYAR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSKYAR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.3%;
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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2.2e+02;
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RESULT 32
ADB06538
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                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                           Query Match
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30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                          This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAX00602) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino acid sequences AAW67807-W68004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypucleotides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 87 polynucleotides, based on which tissues they are most highly expressed in (see AAX00611 for described uses)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Young P, Florence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
WO2003048304-A2
                        Alloiococcus
                                                            Alloiococcus
                                                                                                               20-NOV-2003
                                                                                                                                                                ADB06538 standard; protein; 145 AA
                                                                                                                                                                                                                                                                                                                                     Sequence 139
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19-AUG-1997
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30-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI
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                                                                                                                                                                                                                                                          FSRYAR 6
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KA, Olsen I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 329;
                                                                                                                                                                                                                                                                                    Conservative
                        otitis
                                             otitidis; antigenic protein; immunogenic; Gram-positive bacterium; infection.
                                                                                                                                                                                                                                                                                                                                     A
                                                                                    otitis
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0048187P.
97US-0048188P.
97US-0048351P.
97US-0048352P.
97US-0048355P.
97US-005037P.
97US-0056370P.
97US-0056370P.
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97US-0048099P.
97US-0048131P.
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97US-0048154P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HS,
                                                                                   antigenic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385pp; English.
                                                                                                                                                                                                                                                                                              90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferrie AM,
S, Ebner R,
                                                                                                                                                                                                                                                                                 Score 28; DB 2;
Pred. No. 2.3e+02;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM, 1
Brewer LA,
                                                                                      SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA, Lu
                                                                                      NO:478
                                                                                                                                                                                                                                                                                  <u>,</u>
                                                                                                                                                                                                                                                                                                           Length 139
                                                            immunisation;
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A, Shi Y;
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                                                                                                                                                                                                                                                                                  Gaps
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RESULT 33 ADB06540

ADB06540 standard; protein; 172

밁 S

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Alloiococcus

Alloiococcus otitidis; antigenic protein; immunogenic; immunisation;

Gram-positive bacterium; infection

otitis antigenic protein SEQ ID NO:480.

(first entry)

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CC expression vector comprising the novel isolated polynucleotide (1), its complement, degenerate variant or fragment; (3) a genetically engineered (2) (2) an antibody specific for the polypeptide of (1); (5) an immunogenic (4) an antibody specific for the polypeptide of (1); (5) an immunogenic (5) (6) a pharmaceutical composition comprising the polypeptide, its complement, biological (5) (6) a pharmaceutical composition comprising the polypeptide of (1) and a carrier; (7) a protein chip comprising an array of the polypeptides of (1), their biological equivalent or fragment; (8) (6) a pharmaceutical composition comprising an array of the polypeptides of (1), their biological equivalent or fragment; (8) (7) a protein chip comprising an array of the polypeptides of (1), their biological equivalent or fragment; (8) (8) immunising against Alloicoccus otitidis by administering to a host the contitudes in the biological sample; (10) a kit comprising a container (8) (9) detecting and/or identifying Alloicoccus otitidis in the biological sample; (10) a kit comprising a container (10) or the antibody of (4); and (11) producing a polypeptide by culturing the genetically engineered host cell under conditions suitable to produce the polyputides, polypeptides, antibodies and compositions of the present convention can be used for treating and diagnosing diseases, drug (10) screening assays and monitoring of effects during drug clinical trials. The present sequence represents an Alloicoccus otitidis outlidis. The present sequence represents an Alloicoccus otitidis
Query Match
Best Local S
Matches 5
                                                                                     Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 33; SEQ ID NO 478; 1019pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Alloiococcus otitidis polynucleotides and polypeptides, treating and diagnosing diseases, drug screening assays and effects during drug clinical trials.
                                                                                                                               antigen protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an isolated polypeptide that is encoded by the polynucleotide (I); (2) an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alloiococcus otitidis genomic DNA, which encodes an antigenic protein Alloiococcus otitidis is a Gram-positive bacterium. Also described: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fletcher LD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-NOV-2001;
18-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-NOV-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated polynucleotide
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Similarity
5; Conserv
  Conservative
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2002US-0426742P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mcmichael JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOLDINGS
                      90.3%;
Score 28; DB 6;
Pred. No. 2.4e+02;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Russell DP,
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      0
                                          Length 145
      Indels
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AAW67842
ID AAW6
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KW Huma
KW diag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC composition comprising the polypeptide, its complement, biological CC equivalent or fragment, or the polypeptide, its comprised in the CC expression vector; (6) a pharmaceutical composition comprising the CC expression vector; (6) a pharmaceutical composition comprising the CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array of the polypeptides of (1), their biological equivalent or fragment; (8) continuous composition; (9) detecting and/or identifying Alloicoccus otitidis by administering to a host the immunogenic composition; (9) detecting and/or identifying Alloicoccus otitidis in the biological sample; (10) a kit comprising a container containing the novel polymucleotide, its degenerate variant or fragment, CC or the antibody of (4); and (11) producing a polypeptide by culturing the genetically engineered host cell under conditions suitable to produce the CC polymucleotides, polypeptides, antibodies and compositions of the present CC invention can be used for treating and diagnosing diseases, drug corrections assays and monitoring of effects during drug clinical trials. The present sequence represents an Alloicoccus otitidis. The present sequence represents an Alloicoccus otitidis.
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                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes an isolated polynucleotide (I) of Alloiococcus ottitidis genomic DNA, which encodes an antigenic protein. Alloiococcus ottitidis is a Gram-positive bacterium. Also described: (1) an isolated polypeptide that is encoded by the polynucleotide (I); (2) an expression vector comprising the novel isolated polynucleotide (I); its complement, degenerate variant or fragment; (3) a genetically engineered host cell, transfected, transformed or infected with the vector of (2); (4) an antibody specific for the polypeptide of (1); (5) an immunogenic composition comprising the notward of the composition of the polypeptide of (1); (5) an immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring effects during drug clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-2001; 2001US-0333777P.
18-NOV-2002; 2002US-0426742P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 33; SEQ ID NO 480; 1019pp; English.
Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
                                                                                                                                                                                          AAW67842 standard; protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003048304-A2
                                                                 Human secreted
                                                                                                                                                  AAW67842
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                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                       (first entry)
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                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                    90.3%;
83.3%;
                                                             encoded by gene 36 clone HODCL36.
                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 6;
Pred. No. 2.9e+02;
1; Mismatches (
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                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Length 172;
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30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
05-AUG-1997;
19-AUG-1997;
02-OCT-1997;
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30-MAY-1997;
30-MAY-1997;
                This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAX00602) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 87 novel genes and their fragments (nucleic acid sequences: AAX00611-X00724; amino acid sequences AAA67807-M68004) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypucleotides. Specific uses are described for each of the 87 polynucleotides, based on which tissues they are most highly expressed in a sample or any second contact in the second cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obseity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-1997
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30-MAY-1997
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21-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 291; 385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAX00646.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME
AAX00611 for
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97US-0048355P.
97US-0050937P.
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97US-0048154P.
97US-0048160P.
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97US-0060862P
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97US-0048188P.
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    described uses)
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S, Ebner R,
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Brewer LA,
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Shi Y;
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Query Match Best Local S Matches 5

Similarity 83.: 5; Conservative

90.3%;

Score 28; DB 2; Le Pred. No. 2.9e+02; 1; Mismatches 0;

Length 174;

Indels

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Sequence

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RESULT 35
ADY14896
 RESULT 36
AEP69875
ID AEP69
XX AEP69
XX AEP69
XX AEP69
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XX AEP69
XX O6-AF
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                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating ar related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO
                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic; Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic; Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
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   satellite
                        Microsatellite
                                                  06-APR-2006
                                                                           AEF69875
                                                                                                 AEF69875 standard; protein;
                                                                                                                                                                                                                                                               Sequence 174
                                                                                                                                                                                                                                                                                     polypeptide
                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID NO 702; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abbas A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-AUG-2003; 2003US-0493546P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-AUG-2004; 2004WO-US026249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antiallergic; ds; gene; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO polypeptide SEQ ID NO 702.
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                                                                                                                                                               FARYAR 74
                                                                                                                                                                                      FSRYAR 6
   DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clark H,
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                             A,
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                                                  (first entry)
tumor marker; therapeutic; diagnosis;
                       instability colorectal tumor marker protein SEQ ID NO:53.
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                                                                                                                                                                                                                         90.3%;
83.3%;
                                                                                                                                                                                                             Score 28; DB Pred. No. 2.9e.
                                                                                                   174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams MP,
                                                                                                                                                                                                         JB ,
2.9e+02;
0;
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                                                                                                                                                                                                                                     Length 174;
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prognosis,
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RESULT 37
AEA17517
ID AEA17
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             instability in an individual by measuring the expression of the sequence of one or more nucleotide sequences defined in the specification, where microsatellite instability is determined as overexpression of the sequence by at least 2-fold compared to the expression in an individual known to not have microsatellite instability. Alternatively the method comprises detecting binding of a ligand to a polypeptide encoded by one or more of the above nucleotide sequences. The methods are useful for detecting microsatellite instability in an individual, for identifying colon tissue having microsatellite instability, for monitoring the onset,
                                                                                                                                                                                                                                                                                                                                                                                                                                   progression, or regression of cancer or a pre-malignant condition in a subject. for determining prognosis for cancer or a pre-malignant condition in a subject. The nucleotides and polypeptides are useful for determining the efficacy of a test compound or a therapy for inhibiting cancer in a subject and for selecting a composition for inhibiting cancer in a subject and for selecting a composition for inhibiting cancer in a subject. The compound, composition and method are useful for treating cancer. This sequence is a protein encoded by a marker DNA sequence specific for a high degree of microsatellite instability (MSI-H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for monitoring the onset, progression, or regression of cancer or a pre-malignant condition, particularly colorectal cancer, in an individual, comprising detecting microsatellite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              colorectal tumor; cancer; neoplasm; cytostatic
                                             Thale cress caleosin-related family protein, SEQ ID NO:
                                                                                28-JUL-2005
                                                                                                                                                      AEA17517 standard; protein; 243
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        marker) relative to colorectal tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 24; SEQ ID NO 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  progression,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thibodeau S,
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13-APR-2005; 2005US-00105233
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                                                                                                                                                                                                                                                                              1 FSRYAR 6
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MAYO FOUND MEDICAL EDUCATION &
                                                                                                                                                                                                                                                                                                               Similarity 5; Conserv
                                                                                                                                                                                                                                             FARYAR 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microsatellite instability, useful for monitoring the onset, on, or regression of cancer, comprises measuring the expressi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Catino TJ,
                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                 90.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burgart L,
                                                                                                                                                                                                                                                                                                               Score 28; DB 10; 1 Pred. No. 2.9e+02; 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                  Length 174;
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                                                 122.
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                                                                                                                                                                                                                                                                                                                   Gaps
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Apolipoprotein; expression; transgenic plant; vascular disease; atherosclerosis; vasotropic;

pharmaceutical;

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antiarteriosclerotic;

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RESULT 38
ABR40670
ID ABR40
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AC ABR40
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DT 16-MZ
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pure oil bodies comprising an apolipoprotein obtained from plants. The nucleic acid sequence capable of controlling expression is a seed-preferred or constitutive promoter such as a phaseolin promoter and a ubiquitin promoter. The chimeric nucleic acid construct additionally comprises a nucleic acid sequence encoding a stabilizing polypeptide linked in frame to the sequence encoding apolipoprotein. It is a plant-specific oil body protein or a thioredoxin (SEQ ID NO: 56). The oil body protein is selected from oleosin, caleosin, and steroleosin. The non-
                                                                                                                                                                                                                                                                                                                                                                                                                            plant specific stabilizing polypeptide is a green fluorescent protein (SEQ ID NO: 57) or a single chain antibody. The single-chain antibody is capable of facilitating purification of appolipoprotein expressed in seeds or is capable of specifically associating with an oil body protein.

Alternatively, the single-chain antibody is a single-chain Fv antibody (SEQ ID NO: 240) capable of associating with the 18 kDa oleosin from A. thaliana (D9scFv). The pharmaceutical apolipoprotein formulation may be used to treat vascular diseases, such as therosclerosis. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression in plant cells; and a sequence encoding an apolitopprotein polypeptide; introducing the chimeric nucleic acid construct into a gcell; and growing the plant cell into a mature plant where the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expressing apolipoprotein in plants which may be used for treating vascular diseases, comprises introducing a chimeric nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-NOV-2003; 2003US-0519606P.
16-JUN-2004; 2004US-0579733P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              caleosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell; and growing the plant cell into a mature plant where the plant expresses apolipoprotein. Also disclosed is a composition of substantially sure apolipoprotein obtained from a plant, or substantially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to methods for expressing apolipoprotein plants by introducing a chimeric nucleic acid construct into a plant cell. Specifically, this comprises providing a chimeric nucleic acid construct comprising a nucleic acid sequence capable of controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 122; 530pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       construct into a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-372355/38
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                   Zea mays oil trait related protein sequence SEQ ID NO:160
                                                         16-MAY-2003
                                                                                                                               ABR40670 standard;
                                                                                                                                                                                                                                                                                                                                                                           Sequence 243
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                                                                                                                                                                                                                                                                                                  Local Similarity nes 5; Conserv
                                                                                                                                                                                                                            159
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                                                                                                                                                                                                                                                                                                                                                                                                                 is a thale cress caleosin protein sequence.
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                                                         (first entry)
                                                                                                                               protein; 244
                                                                                                                                                                                                                                                                                                                    90.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell.
                                                                                                                                                                                                                                                                                                Score 28; DB Pred. No. 4.1e
1; Mismatches
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                                                                                                                                                                                                                                                                                             DB 9;
. 4.1e+02;
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RESULT 39
ADX91903
ID ADX91
XX ADX91
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Best Local Similarity
Thes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                   activated protein (MAP) kinase activity, LIPIS-like transcription factor activity, caleosin-like activity, ATP citrate lyase activity, SNP1-like activity and CKC-like transcription factor activity. Also described: (1) complement (II) of (I); (2) a chimeric construct (III) comprising (I) or (II), operably linked to a regulatory sequence; (3) a plant (IV) comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5) oil obtained from (V). (I) or its part can be used in antisense inhibition or co-suppression in a transformed plant. (III) is useful for altering the oil phenotype in a plant such as corn, soybean, wheat, rice, canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for creating transgenic plants having altered lipid profiles. (I) can also be used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to ABR40879 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Allen SM,
Jones TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase; receptor-like protein kinase; mitogen activated protein kinase; oil; LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1; CKC-like transcription factor; antisense inhibition; co-suppression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleotide fragment encoding polypeptides having receptor-like protein kinase activity, caleosin-like activity, useful for altering phenotypes in plants such as sunflower, coconut, soybean, wheat and i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUN-2001; 2001US-0301913P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising a nucleic acid sequence (NS) chosen from a NS encoding a polypeptide (PP) having receptor-like protein kinase activity, mitogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Page 202-203; 542pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tarczynski
                                                                                                                                                        ADX91903 standard; protein; 256
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an isolated nucleotide fragment (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-201509/19.
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                                                                                                                                                                                                                                                 163 FSKYAR 168
                                                                                                                                                                                                                                                                                  1 FSRYAR 6
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Kinney
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                                                                                        (first entry
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83.3%;
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Klein TM,
                                                                                                                                                                                                                                                                                                                   Score 28; DB 6; Le
Pred. No. 4.2e+02;
1; Mismatches 0;
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Li C, Oliveira IC, Sakai
                                                                                                                                                                                                                                                                                                                                                      Length 244;
                                                                                                                                                                                                                                                                                                                      Indels
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ai H, Shen
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rice
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plant protectant; plant growth regulant; gene therapy; plant;
recombinant DNA construct; physical array; plant breeding marker;

Plant full length insert polypeptide seqid 54567.

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RESULT 40
ABG07163
 BXXXI
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                                                                                                                                                                                                                                      CC polynucleotide consisting of a sequence encoding an amino acid sequence cavailable in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide cof the invention are also useful in physical arrays of molecules and as comproving plant tolerance to cold, heat, drought, herbicides, extrame combination conditions, pathogens or pests, for manipulating growth rate in concreased resistance to plant disease, for manipulating growth rate in cold increased resistance to plant disease, for producing galactomannan, cc lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake cor by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert of invention.
                                                                                                                                                                                  Matches
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA construct, useful for improving plant tolerance cold, heat, drought, herbicides, extreme osmotic conditions, pathoge pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZHOU/)
(KOVA/)
(SCRE/)
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 13-FEB-2002
                           ABG07163;
                                                   ABG07163 standard; protein; 301
                                                                                                                                                                                                                                      Sequence 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 54567; 15pp; English
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05-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               improving yield.
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KOVALIC D K.
SCREEN S E.
                                                                                                                                                                               Similarity 5; Conserv
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                                                                                                                          FSKYAR 179
                                                                                                                                                     FSRYAR 6
                                                                                                                                                                                Conservative
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(first
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 entry)
                                                                                                                                                                                            90.3%;
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                                                                                                                                                                               Score 28; DB
Pred. No. 4.46
1; Mismatches
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                                                                                                                                                                           DB 8;
4.4e+02;
0;
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                                                                                                                                                                                                         Length 256;
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RESULT 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                    patent did not appear in the printed specification,
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences. (I) is useful as hybridisation probes, polymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mappi and in recombinant production of (II). The polymucleotides are also in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 37522; 103pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                       28-JUL-2005
                                                                                                                      AEA17523 standard; protein; 301
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #7154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n; chromosome mapping; gene mapping; gene therapy; forensic;
supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                        FSRYAR 6
                                                                                                                                                                                                                                                                                                                                                                                                   301 AA
                                                                                                                                                                                                                                                                                                                  Conservative
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                                       (first entry)
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                                                                                                                                                                                                                                                                                                               Score 28; DB 4; Le
Pred. No. 5.2e+02;
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                                                                                                                                                                                                                                                                                                                    Gaps
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Thale cress caleosin-1 protein,

SEQ ID

NO: 128

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RESULT 42
AEA17522
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                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 128; 530pp; English.
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16-JUN-2004; 2004US-0579733P.
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                                                                                                                                                                                                                                                                                                                                               Sequence 301
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28-JUL-2005
                                        AEA17522;
                                                                           AEA17522 standard; protein; 301
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                                                                                                                                                                                220 FSKÝÁR 225
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(first entry)
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Pred. No. 5.2e
1; Mismatches
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ABG27724
ID ABG2
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AC ABG2
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                                                                         RESULT 43
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plants by introducing a chimeric nucleic acid construct into a plant cell. Specifically, this comprises providing a chimeric nucleic acid construct comprising a nucleic acid sequence capable of controlling expression in plant cells; and a sequence encoding an apolipoprotein polypeptide, introducing the chimeric nucleic acid construct into a plant cell; and growing the plant cell into a mature plant where the plant expresses apolipoprotein. Also disclosed is a composition of substantially pure apolipoprotein obtained from a plant, or substantially pure oil bodies comprising an apolipoprotein obtained from plants. The nucleic acid sequence capable of controlling expression is a seed-preferred or constitutive promoter such as a phaseolin promoter and a ubiquitin promoter. The chimeric nucleic acid construct additionally
                                                                                                                                                                                                                                                                                                                 comprises a nucleic acid sequence encoding a stabilizing polypeptide linked in frame to the sequence encoding apolipoprotein. It is a plant-specific oil body protein or a thioredoxin (SEQ ID NO: 56). The oil body protein is selected from oleosin, caleosin, and steroleosin. The non-plant specific stabilizing polypeptide is a green fluorescent protein (SEQ ID NO: 57) or a single chain antibody. The single-chain antibody is capable of facilitating purification of apolipoprotein expressed in seeds or is capable of specifically associating with an oil body protein. Alternatively, the single-chain antibody is a single-chain from A. Stabiliana (1995CFV). The pharmaceutical apolipoprotein formulation may be used to treat vascular diseases, such as atherosclerosis. The present sequence is a thale cress caleosin protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressing apolipoprotein in plants which may be used for treating vascular diseases, comprises introducing a chimeric nucleic acid construct into a plant cell.
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16-JUN-2004; 2004US-0579733P.
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                                     ABG27724 standard; protein; 499
                                                                                                                                                                                                                                                                                   Sequence 301 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-372355/38
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                                                                                                                                 220 FSKYAR 225
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                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                           Score 28; I
Pred. No. 5.
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ABG27724;

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RESULT 44
ABG29681
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                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) csequences. (I) is useful as hybridisation probes, polymerase chain creaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed used cin diagnostics as expressed sequence tags for identifying expressed used conditions and the polynucleotides are also used cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a completion in tissue, as molecular weight markers and as a food completion of the expressing (II). (I) and (II) are useful for treating disorders convolving aberrant protein expression or biological activity. The composible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and camino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this cameno activity from the printed specification, but was obtained in celetronic format directly from MIPO at
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-00649167.
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 18-FEB-2002
                               ABG29681;
                                                          ABG29681 standard; protein; 520 AA
                                                                                                                                                                                                                                                                        Sequence 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 58083; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity.
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food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                         FSRYAR 6
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(first entry)
                                                                                                                                                                                                                        90.3%;
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                                                                                                                                                                                                       Score 28; DB 4; Le
Pred. No. 8.7e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                       Length 499;
                                                                                                                                                                                                            Indels
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RESULT 45 ADN18185

ADN18185 standard; protein; 681

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BXAXXX

ADN18185; 02-DEC-2004

(first entry)

Bacterial polypeptide #838

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                                                                            Matches
                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                        polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                genes. (1) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also use in diagnostics as expressed sequence tags for identifying expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                        Sequence 520 AA;
                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                  involving aberrant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 60040; 103pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US008631
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supplement; medical imaging; diagnostic; genetic disorder.
46 FNRYAR 51
                                      1 FSRYAR 6
                                                                            5.
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                    protein expression or biological activity.
                                                                                                90.3%;
83.3%;
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                                                                            1; Mismatches
                                                                                              Score 28; DB 4;
Pred. No. 9e+02;
                                                                            ٠,
                                                                                                                  Length 520;
                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutations
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CC comprising the recombinant DNA construct and a method of producing a crop plant comparising the recombinant DNA construct and a method of producing a crop plant construct and specific as the plant is a crop plant construct and property. The plant is a crop plant converged as the property of producing a transformed plant construct and growing the transformed plant, where the complynucleotide or polypeptide is useful for improving plant, where the construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with the construct is useful for producing plants with the construct is useful for producing plants with the construct is useful for producing plants with construct producing plants with plant growth regulators, increased rate of the cell cycle pathway with plant growth regulators, increased rate of condition, improved yield by modification of carbohydrate, nitrogen or content, improved yield by modification of carbohydrate, nitrogen or condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved lighth production or improved galactomanan construction. Note: The sequence carial polypeptide used in the growth from HEBPTO at gendard near conformation but was obtained in electronic form part form HEBPTO at gendard near conformation but was obtained in electronic conformation.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2002; 2002US-0360039P
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                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a recombinant DNA construct comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 838; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GOLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SLAT/)
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515
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) SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                                                      from USPTO at seqdata.uspto.gov/sequence.html.
                                                                      1 FSRYAR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hinkle GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOLDMAN B
                                                                                                                                      Similarity 5; Conser
                                                                                                                                                                                                                                                                                   681
FARYAR 520
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                   A
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                                                                                                                                                                           90.3%;
                                                                                                                                         1;
                                                                                                                                                                           Score 28; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen
                                                                                                                                                 Mismatches
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                                                                                                                                                                           DB 8;
1.2e+03;
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                                                                                                                                                                                                            Length 681;
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RESULT 46 ABG04036

ABP76771

standard; protein; 1206

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RESULT 47
ABP76771
ID ABP76
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                                                                                                                                                                                                                                                                                                                               cc genes. (I) is useful in gene therapy techniques to restore normal cc activity of (II) or to treat disease states involving (II). (II) is considered in tissue, as molecular weight markers and as a food cc golypeptide in tissue, as molecular weight markers and as a food cc supplement. (II) and its binding partners are useful in medical imaging consistes expressing (II). (I) and (II) are useful for treating disorders convolving aberrant protein expression or biological activity. The cc polypeptide and polynucleotide sequences have applications in convolving aberrant protein expression or biological activity. The cc polypeptide and polynucleotide sequences have applications in convolving aberrant protein expression or biological activity. The cc and to produce other types of data and products dependent on DNA and can be produced other types of data and products dependent on DNA and camino acid sequences. ABG00010-ABG30377 represent novel human diagnostic camino acid sequences of the invention. Note: The sequence data for this camino acid sequences of the printed specification, but was obtained in content of the printed specification of the sequence data for this camino acid sequences of the printed specification, but was obtained in content content this part camino acid sequences of the printed specification.
                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also use in diagnostics as expressed sequence tags for identifying expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US008631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes. polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS68223.
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                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_
                                                                                                                                                                                                                 Local
                                                                                                                                                                                                Similarity 5; Conser
                                                                                                                                                                                                                                                                                 847
                                                                                                                                                           FSRYAR 6
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                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                               AA;
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                                                                                                                                                                                                Score 28; DB 4;
Pred. No. 1.5e+03
1; Mismatches
                                                                                                                                                                                                                       5e+03;
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                                                                                                                                                                                                                                        Length 847;
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RESULT
ABP7868
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Best Local
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                                                                                                                            z
                                                                                                                                                                                                                                                                                                                                                                                                                        New protein from Neisseria medicament for treating or
                12-FEB-2001; 2001GB-00003424.
                                 12-FEB-2002;
                                                    10-OCT-2002
                                                                       WO200279243-A2
                                                                                        Neisseria gonorrhoeae
                                                                                                          Antibacterial;
                                                                                                                                              07-MAR-2003
                                                                                                                                                                 ABP78681
                                                                                                                                                                                ABP78681 standard; protein; 1206 AA
                                                                                                                                                                                                                                                                                                      Sequence 1206 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 182; 815pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fontana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-2001;
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(CHIR-)
                                                                                                                                                                                                    48
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                                                                                                                           gonorrhoeae
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)B; ABZ37741.
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CHIRON
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                                                                                                                                                                                                                               FARYAR 944
                                                                                                                                                                                                                                                FSRYAR 6
                                                                                                                                                                                                                                                                  Conservative
                                   2002WO-IB002069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pizza M,
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                                                                                                                                              (first entry)
SPA
                                                                                                          infection; vaccine;
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                                                                                                                           amino acid
                                                                                                                                                                                                                                                                          90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Masignani
                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         gonorrheae,
preventing
                                                                                                                                                                                                                                                                          Score 28;
Pred. No.
                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                           SEQ
                                                                                                         gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monaci
                                                                                                                                                                                                                                                                                                                                                                                                                          N. gonorrheae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for the manufacture of
                                                                                                                                                                                                                                                                           2.1e+03;
                                                                                                                            ID 3892.
                                                                                                                                                                                                                                                                                   DB 6;
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                                                                                                                                                                                                                                                                  0;
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RESULT 49
ABO69413
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins ar antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of
                                                                                                             Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New protein from Neisseria medicament for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                     Rubenfield MJ,
                                                                                                                                                                                                                                                      18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                           US6551795-B1
                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                           Bacterial infection; Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABO69413;
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                                                                                                                                                                                                                              (GENO-) GENOME
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                                                                                                                                                                  ABD02984.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; protein; 1778 AA.
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                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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98US-0094190P
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                                                                                       18159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gonorrheae, useful preventing N. gonor
                                                                                                                                                                                                     Deloughery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28;
Pred. No.
                                                                                     455pp;
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                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monaci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6,
2.1e+03;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gonorrheae infection
                                                                                                                                                                                                       Bush
                                                                                                                                                                                                                                                                                                                                                                                              infection; antibacterial.
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RESULT 50
ABB78221
ID ABB78
XX ABB78
XX ABB78
XX Zebra
KW Zebra
KW Abart
XX Danic
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                                                                                                The present sequence represents a zebrafish alphalC subunit of a voltage-dependent I-type calcium channel. The specification describes a method for determining whether a test subject has or is at risk of developing a disease or condition related to the alphalC subunit. The method involves analysing a nucleic acid molecule sample from the test subject to determine whether the test subject has a mutation in a gene encoding the alphalC subunit, where the presence of a mutation indicates that subject has or is at risk of developing the disease. The method is useful for determining whether a test subject (preferably mammal e.g. human) has, or is at risk of developing, a disease or condition related to the alphalC, is a trisk of developing, a disease or condition related to the alphalC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining whether a subject has or is at risk of developing disease related to alphalC subunit of voltage-dependent L-type calcium channel, by detecting mutations in genes encoding the subunit in sample of
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RESULT 2 C72022 UDP-N-acetylglucosamine-N-acetylmuramyl- (pentapeptide)	Qy 1 FSRYAR 6        Db 80 FSRYAR 85	Query Match 100.0%; Score 31; DB 2; Best Local Similarity 100.0%; Pred. No. 14; Matches 6; Conservative 0; Mismatches	MIPAC: P76081; UNIPARC: UPI0000 MIPROT: P76081; UNIPARC: UPI0000 s: strain K-12; substrain MG165 slectron transfer; iron-sulfur ansmembrane #status predicted « rredoxin [2Fe-2S] homology «PER nding site: 2Fe-2S cluster (Cys	au, B.; Shao, 1462, 1997 ste genome se : A64720; MUII ) acid sequence NA	tron transfer protein - Cherichia coli p-1997 #sequence_revisic C64990 R.; Plunkett III, G.; E	ALIGNMENTS	23 74.2 366 23 74.2 366 23 74.2 366 23 74.2 366 23 74.2 367	23 74.2 360 2 23 74.2 360 2 23 74.2 361 1 23 74.2 361 1 23 74.2 362 2 23 74.2 362 2	23 74.2 360 1 23 74.2 360 2 23 74.2 360 2 23 74.2 360 2 23 74.2 360 2	23 74.2 358 2 23 74.2 358 2 23 74.2 359 2 23 74.2 359 2 23 74.2 360 1	74.2 350 2 23 74.2 350 2 23 74.2 351 2 23 74.2 352 2 352 2 74.2 356 2 23 74.2 356 2	00000000
tide) pyrophosphoryl-undecaprenol N-ace		; Length 356; 0; Indels 0; Gaps 0;	013119E; GB:AE000236; GB:U00096; NID:gJ 55 tochrome-b5 reductase homology; ferredc protein; metalloprotein; transmembrane <pre><pre><pre><pre><pre><pre><pre><pre></pre></pre></pre></pre></pre></pre></pre></pre>	ia coli K-12. 78503 Lion not shown	Escherichia coli (strain K-12) nn 17-Sep-1997 #text_change 05-Oct-2004 sloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col		hypothetical prote hypothetical prote translation releas ribonucleoprotein translation releas	פסאס	ion rechain chain chain	(0 ) (4)	hypothetical 33.7K hippocampal 38K au unknown protein (i hypothetical prote translation releas translation releas	RNA-binding protei hypothetical prote hypothetical prote translation releas hypothetical prote protein T30E16.21 ribonucleoprotein conserved hypothet

## ALIGNMENTS

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I:P76081; UNIPARC:UPI000013119E; GB:AE000236; GB:U00096; NID:glain K-12, substrain MG1655
ioxygenase reductase; cytochrome-b5 reductase homology; ferredon transfer; iron-sulfur protein; metalloprotein; transmembrane status predicted <TM01>
in [2Fe-2S] homology <FER>
site: 2Fe-2S cluster (Cys) (covalent) #status predicted
100.0%; Score 31; DB 2;
100.0%; Pred. No. 14;
10e 0; Mismatches 0
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shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NO Sequence of Escherichia coli K-12. MUID:97426617; PMID:9278503
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                                                                                                                                                                                                                                                                                                                                                                            ence not shown; translation not shown
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                                                  Length 356;
  Indels
  0; Gaps
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N;Alternate names: peptidoglycan transferase
C;Species: Chlamydophila pneumoniae, Chlamydi
C;Date: 23-Apr-1999 #somronomiae
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A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935
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A; Cross-references: UNIPROT: Q9Z702; UNIPARC: UPI00000470A7;
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R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptidoglycan transferase [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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A;Experimental source: strain AR39, HL cells
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                    probable proline transport protein - Bacillus subtilis
N;Alternate names: probable proline-specific permease
C;Species: Bacillus subtilis
                                                                                            C69997
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C;Superfamily: murG
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#sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertert C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi A.; Ehrlich, S.D.; Emmerson, P.T.; Ehrlian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogth, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, K.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, R.; Gave, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamamoto, K.; Yasamoto, V.; Uchiyama, A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A., Molecusia, Proper na.
A.; Millors: Foshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.; Status: preliminary; nucleic acid sequence not shown; translation not shown
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F;203-219/Domain: transmembrane #status predicted <TM6>
F;2040-256/Domain: transmembrane #status predicted <TM6>
F;280-296/Domain: transmembrane #status predicted <TM9>
F;380-352/Domain: transmembrane #status predicted <TM9>
F;336-352/Domain: transmembrane #status predicted <TM9>
F;361-377/Domain: transmembrane #status predicted <TM10>
F;404-420/Domain: transmembrane #status predicted <TM11>
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Mol. Biol. Evol. 9, 688-706, 1972
A; Title: Nucleotide sequence, function, activation, and nucleotide sequence, function, activation, and nucleotide sequence, MUID:92334140; PMID:1630307
                                                                                                                                                                                                                                                                                                                                    Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12
A;Reference number: A64720; MUID:97426617; PMID:9278503
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C;Superfamily: ecotropic retrovirus receptor protein
C;Keywords: amino acid transport; transmembrane protein
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A;Cross-references: UNIPROT:034618; UNIPARC:UPI0000060942; GB:Z99119; GB:AL009126; NID:g'
A;Experimental source: strain 168
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                                                                                                        R;Hall, B.G.; Xu,
                                                                                                                                              A;Cross-references: UNIPROT:P24240;
A;Experimental source: strain K-12;
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A; Residues: 1-474 <BLAT>
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                                                                         9, 688-706, 1<u>9</u>92
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Pred. No.
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R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; xokoyama, k.; ngasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7

A.Reference number: A99629; MUID:21156231; PMID:11258796

A.Accession: D91075
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A;Cross-references: UNIPARC:UPI000016EE0A; GB:M73326; NID:g145385; PIDN:AAA16430.1;
A;Experimental source: strain LP103
A;Note: sequence extracted from NCBI backbone (NCBIN:109109, NCBIP:109114)
C;Genetics:
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                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-474 <STO>
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C;Superfamily: Agrobacterium beta-glucosidase
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A; Residues: 1-474 <HAY>
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h 100.0%;
Similarity 100.0%;
6; Conservative 0
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                                                                        Agrobacterium beta-glucosidase
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Pred. No. 18;
0; Mismatches
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                  Score 31;
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Mismatches 0
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K.; Apodaca,
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   C;Accession:
R;Chissoe, S
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A; Residues: 1-239 < HS
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R;Hsu, T.F.; Tsai,
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C;Superfamily:
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A; Residues: 1-496 <STO>
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                                                                                           T16828
                                                                                                            RESULT 10
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hypothetical protein T07F12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #tey C;Date: 20-Sep-1999 #tey C;Accession: T16828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ca+2-binding EF hand protein homolog PM13 - soybean C;Species: Glycine max (soybean) C;Decies: Glycine max (soybean) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004 C;Accession: T07092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: B83591
R;Stover, C:K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, and A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, and A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, and A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, and A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, and A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, and A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, and A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, and A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, and A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, and A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, and A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, ar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: PM13
C;Superfamily: rice abscisic acid-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, May 1997 A;Description: Glycine max mRNA for Ca+2-binding EF-hand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:023959; UNIPARC:UPI00000A8419; EMBL:AF004809; NID:g2270993; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain Shi-shi; cotyledon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z15913
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262
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                                                                                                                                                                                                                                                                                                                                                                                                             90.3%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28;
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    Pseudomonas aeruginosa

                             20-Sep-1999 #text_change 09-Jul-2004
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K.; Lim,
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probable allantoin permease [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sommore-
                                A; Molecule type: DNA
A; Residues: 1-437 < KUR>
A; Residues: 1-437 < KUR>
A; Residues: 1-437 < KUR>
A; Cross-references: UNIPROT: Q92X34; UNIPARC: UPI00000CB40E; GB: AL591985; PIDN: CAC48528.1.
A; Experimental source: strain 1021, megaplasmid pSymB
A; Experimental source: strain 1021, 
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A; Map position: I
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A;Molecule type: DNA
A;Residues: 1-409 <KUR>
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R;DelVecchio, W.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688

A;Accession: AF3271
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A; Residues: 1-304 < CHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                     R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing enda A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable deaminase protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmic
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 31-Dec-2004
C;Accession: H95857
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    A;Authors: Kahn, D.; Kahn, M.L.; Kalman,
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;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
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methionyl-trnA synthetase (metS) [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C;Accession: D90202 C;Rccession: D90202 C;R;She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redd arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001 A;Description: Sulfolobus solfataricus complete genome. A;Reference number: A99139 A;Accession: D90202
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A;Rolecule type: DNA
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A;Residues: 1-475 <KUR>
A;Residues: 1-475 <KUR>
A;Cross-references: UNIPROT:Q92YG7; UNIPARC:UPI00000CB248; GB:AE006469; PIDN:AAK65571.1;
A;Experimental source: strain 1021, megaplasmid pSymA
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A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: A95376
A;Status: preliminary
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A;Status: preliminary A;Molecule type: DNA
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Han,

C.G.

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dipeptidyl carboxypeptidase II [imported] - Escher: C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 C;Accession: C90897
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A; Residues: 1-138'LL',141-681 <HEN>
A; Cross-references: UNIPARC: UPI000016F0BD;
A; Becker, S.; Plapp, R.
submitted to the EMBL Data Library, Februar
A; Reference number: S14870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 12-Sep-1997 #sequence revision 17-Sep-1997 #text_change 09-Jul-2004 C;Accession: E64908; A49931; S14870 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; l. A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                       RESULT
C90897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: catalyzes hydrolysis of unblocked C-terminal dipe;
A;Note: zinc cofactor
C;Superfamily: peptidyl-dipeptidase Dcp
C;Keywords: metalloproteinase; peptidyldipeptide hydrolase; zinc
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C;Superfamily: methionyl-tRNA synthetase
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A;Cross-references: UNIPARC:UPI000016F0BD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
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Pred. No. 1.1e+02;
1; Mismatches 0
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Pred. No. 1.3e+02;
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                                                                                                 Escherichia coli (strain 0157:H7,
                           #text_change
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          A;Residues: 1-877 <KUR>
A;Residues: 1-877 <KUR>
A;Cross-references: UNIPROT;Q8YS49; UNIPARC:UPI00000CE703;
                                                                                                                                                                                                  DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic ScA;Reference number: AB1807;
A;Accession: AC2211
                                                                                                                                                                                                                                                                                                C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 C;Accession: AC2211
C;Ac
A; Experimental source: C; Genetics:
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                                                                                                                                   A; Molecule type:
                                                                                                                                                                   A;Status: preliminary
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18

(strain PCC

DNA

GB:BA000019; PIDN:BAB74941.1;

Sequence of the Filamentous Nitrogen-fixing 7; MUID:21595285; PMID:11759840

Cyanobacterium

Anat ß

, A.;

Tabata,

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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D85720
C;Accession: D85720
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: C90897
                                                                                                                                               A;Gene: dcp
C;Superfamily:
                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q8XB30; UNIPARC:UPI00000D0637; A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                  A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551
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C;Species:
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5; Conserve
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Pred. No. 1.3e
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Pred. No.
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1.3e+02;
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Potamousis,
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C;Accession: D83181

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, i Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

Nature 406, 959-964, 2000
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A; Residues: 1-36 < STO>
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A;Cross-references: UNIPROT:Q9HXR4; UNIPARC:UPI00000C5AE2;
A;Experimental source: strain PAO1
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AI0982
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Pred. No.
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A.; Larbig,
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K.; Lim,
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A; Title: The Genome A; Reference number: A; Accession: AH2740
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C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AIO982 C;Accessio
                                                                                                        Conserved hypothetical protein Atul336 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C;Accession: AH2740 C;Accession: AH2740 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001 Science 294, 2317-232
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C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change
C;Accession: F97521
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C;Genetics:
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A; Residues: 1-43 < PAR >
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                                                                                 A; Authors: ster, E.W.
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A;Reference number: A97359; MUID:21608551; PMID:11743194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSRYAR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FERYAR
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of the Natural Genetic Engineer Agrobacterium tumefaciens C58 AB2577; MUID:21608550; PMID:11743193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
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83.3%;
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Pred. No.
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37;
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                                                                                                                              W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skelton, J.; Stevens, K.; Salmonella enterica serova
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; Lappas, C.;
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Markelz,
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kelz, B.;
                                                                                                                                                                                                                                                             , Woo, L.
McClella
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A;Gene: guk
A;Gene: guk
A;Introns: 25/1; 80/3; 83/1; 173/2
A;Introns: 25/1; 80/3; 83/1; 173/2
C;Superfamily: mucleoside diphosphate kinase
C;Keywords: ATP binding; hexamer; mitochondrion; phosphohistidine; phosphoprotein;
C;Keywords: ATP binding #status predicted
F;83-87/Region: ATP binding #status predicted
F;186/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleoside-diphosphate kinase (EC 2.7.4.6) precursor, mitochondrial - slime C;Species: DictyOstelium discoideum C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 05-Oct-2004 C;Accession: B49547 R;Troll, H.; Winckler, T.; Lascu, I.; Mueller, N.; Saurin, W.; Veron, M.; M. J. Eigl. Chem. 268, 25469-25475, 1993
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                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-220 <TRO>
A; Cross-references: UNIPARC: UPI0000175708;
C; Genetics:
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B49547
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-108 < KUR>
A;Residues: 1-108 < KUR>
A;Cross-references: UNIPROT:Q8UFR1; UNIPARC:UPI00000D1B08; GB:AE008688; PIDN:AAL42342.1.
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A;Molecule type: DNA
A;Residues: 1-208 <STO>
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, N.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Goi
                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C;Accession: AE3245
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C; Superfamily: 1
C; Keywords: cyto
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A;Cross-references: UNIPARC:UP10000133CD5; EMBL:AL035077; PIDN:CAA22664.1; GSPDB:GN00066; A:Experimental source: strain 972h-; cosmid c18E5
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A;Reference number: Z21878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Masson, J.Y.; Vadnais, J.; Ramotar, D. Gene 170, 153-154, 1996
A;Tille: The Schizosaccharomyces pombe spqM gene is a new A;Reference number: JC4755; MUID:96200877; PMID:8621081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Schizosaccharomyces pombe
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change
C;Accession: JC4755; T39755
                                                                   A;Genome: plasmid
C;Superfamily: ol:
                                                                                                                                                   A;Cross-references: UNIPROT:Q8U604; A;Experimental source: strain C58 ()
                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-286 < KUR>
                                                                                                                                                                                                                                                                            A; Title: The Genome of the Natural Genetic Engineer Agrobacterium A; Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                     A; Authors: Yoo, H.; ster, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein accE [imported] - C;Species: Agrobacterium tumefaciens
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A; Residues: 1-232 < MAS>
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es, S.
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Local Similarity

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dTDP-4-dehydrorhamnose reductase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: E87697
C;Accession: E87697
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                 RESULT
E87697
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A; Residues: 1-286 < P
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A; Accession: T03434
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C;Date: 24-Mar-1999 #sequence revision 24-Mar-1999
C;Accession: T03434
R;Piper, K.R.; Beck von Bodman, S.; Cook, D.M.; Hwa
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A;Description: Identification of a cryptic proline transport system
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C;Superfamily: oligopeptide permease protein
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A;Residues: 1-292 <LIA>
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A;Gene:
C;Superf
C;Keywor
                                                                                                                                                                                                                                                               polyketide synthase (EC 2.-...) chain 6 - Actinomadura hibisca C;Species: Actinomadura hibisca C;Species: Actinomadura hibisca C;Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004 C;Accession: JC5855 R;Dairi, T.; Hamano, Y.; Igarashi, Y.; Furumai, T.; Oki, T. Biosci. Biotechnol. Biochem. 61, 1445-1453, 1997 Biosci. Biotechnol. Biochem. 61, 1445-1453, 1997 A;Title: Cloning and nucleotide sequence of the putative polyketide synthase A;Reference number: JC5850; MUID:97480928; PMID:9339544 A;Accession: JC5853
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A;Residues: 1-293 <STO>
A;Cross-references: UNIPROT:Q9A2FO; UNIPARC:UPI00000C7B37; GB:AE005673; NID:g13425365; PJ
C;Genetics:
A;Gene: CC3615
C;Superfamily: dTDP-dihydrostreptose synthase
                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-341 <DAI>
A;Residues: 1-341 <DAI>
A;Cross-references: UNIPROT:032456; UNIPARC:UPI000002F07D; DDBJ:D87924; NID:g2580441;
C;Comment: This enzyme catalyzes repeated condensation cycles of acyl-CoA, affecting t
C;Genetics:
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N;Alternate names: protein F4P12.200
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change
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T45890
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A;Introns: 36/2; 41/3; 67/3; 99/3; 164/2; 198/2
A;Note: F4P12.200
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A; Residues: 1-302 <BLO>
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A;Accession: T45890
A;Status: preliminary
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Matches 5
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Best Local
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83.3%;
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C;Species: Beeudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Date: no. C83575
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hicladman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lar.; Lory, S.; Olson, M.V.
 M.; Ohfu
DNA Res.
A; Title:
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C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999
C;Accession: E75080
R;anonymous, Genoscope
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C;Genetics:
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Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C83575
                                                              probable phosphoglycerate kinase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Aug-2004
C;Accession: D71065
                                                                                                                                                                                                                                                                                                 A;Gene: PAB1679
C;Superfamily: phosphoglycerate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, July 1999 A;Description: Pyrococcus abyssi genome sequence: A;Reference number: A75001 A;Accession: E75080
              R;Kawarabayasi, Y.; Sawada, M.; Ohfuku, Y.; Funahashi, DNA Res. 5, 55-76, 1998
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C;Superfamily:
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A; Residues: 1-354 <STO>
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A; Residues: 1-410 <KAW>
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C;Species: Pseudomonas aeruginosa
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83.3%;
   and
                               M.; Horikawa
T.; Tanaka,
 gene
                             Horikawa, H.; Haikawa, Y.; Hino, Tanaka, T.; Kudoh, Y.; Yamazaki,
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J.; Kushida, N.;
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A.; Larbig,
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C; Superfamily:
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A; Residues: 1-453 <S'
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A; Residues: 1-411 < DUZ >
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   Query Match
Best Local
                                             Gene: CC3414
Superfamily:
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Best Local
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A,Status: preliminary; nucleic acid sequence not shown; tra A;Molecule type: DNA A;Residues: 1-410 <KAN> A;Residues: 1-410 <KAN> A;Cross-references: UNIPROT:058965; UNIPARC:UPI000013180B; A;Experimental source: strain OT3 A;Note: this accession replaces an interim accession for a C;Genetics:
                                                                                                                                                                                                                                                                                            R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolong n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, July 1995 A; Description: sequence of C. elegans cosmid A; Reference number: S59417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein C30B5.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Deceies: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 C;Accession: T15705
                                                                                                                                                                                                                                                A; Reference number: A87249; MUID:21173698; PMID:11259647 A; Accession: D87672
                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
C;Accession: D87672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glutamate-cysteine ligase [imported] -
C;Species: Caulobacter crescentus
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A;Introns: 12/2; 91/1; 349/3
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                                                                     glutamate--cysteine ligase
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th, T.; Commonder, P.
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Title: Complete ABD502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT: P77327; UNIPARC: UPI000013232F; A;Experimental source: strain K-12, substrain MG1655 C;Superfamily: ecotropic retrovirus reptor protein C;Keywords: amino acid transport; transmembrane protein E;43-59/Domain: transmembrane #status predicted <TM1> F;96-112/Domain: transmembrane #status predicted <TM2> F;15-11/Domain: transmembrane #status predicted <TM4> F;15-173/Domain: transmembrane #status predicted <TM4> F;241-257/Domain: transmembrane #status predicted <TM4> F;241-257/Domain: transmembrane #status predicted <TM4> F;241-257/Domain: transmembrane #status predicted <TM5> F;241-257/Domain: transmembrane #status
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_C;Accession: B64769
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli
A;Reference number: A64720; MUID:97426617; PMID:9278503
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A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C;Accession: AH0551
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A; Residues: 1-456 < PAR>
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C;Superfamily:
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A; Accession: AH0551
                                                                                                                                                                                                                                                      F;279-295/Domain: transmembrane F;330-346/Domain: transmembrane
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transmembrane
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                                               87.1%;
83.3%;
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          probable proline-specific permease [imported] - Yersinia C;Species: Yersinia pestis C;Jate: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_C;Date: 01-Nov-2001 #sequence_revision 02-Nov-2001 #text_R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball. R.W.:
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AI0388
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proline permease transport protein [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;Accession: H8553
C;Accession: H8553
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.;
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Application of Ecological Colors (Color) (Color)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proline permease transport protein ECs0452 [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C;Accession: D90685
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C; Superfamily:
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A;Cross-references: UNIPROT:P77327; UNIPARC:UPI000013232F;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: H8535 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iller, L.; Grotbeck, E.J.
Nature 409, 529-533, 2001
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C;Superfamily:
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DNA Res. 6, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A·Reference number: A99629; MUID:21156231; PMID:11258796
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N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; S
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75 FSRYAQ 80
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83.3%;
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Pred. No.
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#sequence\_revision 02-Nov-2001 #text\_change

pestis

R.W.; Holden, M.T.G.; Prentice,

. B.;

05-Oct-2004 (strain CO92)

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R;el Hassouni, M.; Henrissat, B.; Chippaux, M.; Barras, F.
J. Bacteriol. 174, 765-777, 1992
A;Title: Nucleotide sequences of the arb genes, which control beta-glucoside utilization clase family including enzymes from eubacteria, archeabacteria, and humans.
A;Reference number: A42603; MUID:92121114; PMID:1732212
A;Accession: C42603
                                                                                                                                                                                                                  R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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C;Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-465 <EL1>
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C;Species: Erwinia chrysanthemi
C;Species: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C;Date: 04-Sep-1998
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A;Gene: CC0822
C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                               aldehyde dehydrogenase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
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A; Residues: 1-463 < KUR>
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A;Status: preliminary
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                                                                                  A;Cross-references: UNIPROT:Q9A9Y9; UNIPARC:UPI00000C71A2; GB:AE005673; NID:g13422073;
                                                                                                                A; Residues: 1-478 <STO>
                                                                                                                                     A; Molecule type: DNA
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                                                                                                                                                                 Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                Accession:
                                                                                                                                                                                                                                                                                                                                                                                                    ;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
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83.3%;
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Pred. No. 1.5e+02;
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Pred. No. 1.5e+02;
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A;Cross-references: UNIPROT:Q9Z7V7; UNIPARC:UPI0000043CB3; GB:AE0 A;Experimental source: strain CWL029 A;Experimental source: strain CWL029 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J. C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; Nucleic Acids Res. 28, 1397-1406, 2000 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlam A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide ABC transporter, permease protein, probable CP0151 [imported] - Chlamydophila C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: C72059; B81608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, Nucleic Acids Res. 28, 2311-2314, 2000
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia A;Reference number: A86491; MUID:20330349; PMID:10871362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oligopeptide permease [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: B86565
                                                                                                                                       A; Experimental source: strain C; Genetics:
                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-579 < REA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Comparative genomes of Clamydia pneumoniae and C. A;Reference number: A72000; MUID:99206606; PMID:10192388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: oppC_2
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FSRYVR

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glutamine-fructose-6-phosphate transaminase (isomerizing) N.Alternate names: nodulation protein nodM C.Species: Rhizobium leguminosarum bv. viciae C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_c.Accession: S01040 R.Surin, B.P.; Downie, J.A.
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glutamine-fructose-6-phosphate transaminase N;Alternate names: glucosamine-fructose-6-P C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Se C;Accession: C97575
                                                                                                                                                                                                                                                                                                                           A;Gene: nodM
A;Gene: plasmid pRLiJI
A;Genome: plasmid pRLiJI
C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C;Keywords: aminotransferase; isomerase; nodulation
F;2-608/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status
F;2/Active site: Cys #status predicted
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A;Accession: S01040
A;Molecule type: DNA
A;Residues: 1-608 <SUR>
A;Cross-references: UNIPROT:P08633;
C;Genetics:
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A; Residues: 1-605 < BAE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Note: glucosamine-6-phosphate is used in the biosynthesis of ;Superfamily: glutamine-fructose-6-phosphate aminotransferase
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2/Active site: Cys #status predicted
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                                                            C 2.6.1.16) [misnomer]
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A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; L
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C97575
A;Status: preliminary
A;Molecule type: DNA
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A;Molecule type: DNA
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A;Crose-references: UNIFROT:Q8UEH1;
A;Experimental source: strain C58 (I
C;Genetics:
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan,
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A;Cross-references: UNIPROT:Q8UEH1; UNIPARC:UPI00001643A5;
C;Genetics:
A;Gene: AGR_C_3284
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                      NUCLEOTIDE SEQUENCE [GENOMIC DNA].

STRAIN=W / ATCC 11105;

MEDLINE=98421522; PubMed=9748275; DOI=10.1074/jbc.273.40.25974;

Ferrandez A., Minambres B., Garcia B., Olivera E.R., Luengo J.M.

Garcia J.L., Diaz E.;

"Catabolism of phenylacetic acid in Escherichia coli. Character:

of a new aerobic hybrid pathway.";

J. Biol. Chem. 273:25974-25986 (1998).

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27-APR-2001, integrated into UniProtKB/Swiss-Prot.
01-FEB-1997, sequence version 1
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Probable phenylacetic acid degradation NADH oxido
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
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LinkHub; P76081; -.
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PRINTS; PR00410; PHEHYDRXLASE.

TIGREAMS; TIGR02160; PA_COA_Oxy5; 1.

PROSITE; PS00197; 2FESS_FER_1; 1.

PROSITE; PS51085; 2FESS_FER_2; 1.

2Fe-2S; Complete proteome; Electron transport; FAD; Flavoprotein;
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EMBL; U00096; AAC74474.1; -; Genomic_DNA.

EMBL; D90777; BAA14998.1; ALT_INIT; Genomic_DNA.

EMBL; D90778; BAA15003.1; ALT_INIT; Genomic_DNA.
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                                                                                                     Shirai M., Hirakawa H., Nathori M., Kuhara Shiba T., Ishii K., Hattori M., Kuhara "Comparison of whole genome sequences c from Japan and CWL029 from USA.";
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Q9Z702;
                                                                                                                                                                                                                                                                                Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J.F., Utterback T.R., Berry K.J., Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowma Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F., McClarty G., Salbberg S.L., Bisen J.A., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99206606; PubMed=10192388; DOI=10.1038/7716; Kalman S., Mitchell W.P., Marathe R., Lammel C.J., Fan J., Hyman R Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
01-MAY-1999, sequence version 1.
07-MAR-2006, entry version 36.
UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)
pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
(EC 2.4.1.227) (Undecaprenyl-PP-MurNAc-pentapeptide-UDPG1CNAc)
                                                       NUCLEOTIDE SEQUENCE
STRAIN=TW-183;
Geng M.M., Schuhmach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=murG; OrderedLocusNames=CPn0904, CP0962, Chlamydia pneumoniae (Chlamydophila pneumoniae Bacteria; Chlamydiae; Chlamydiales; Chlamydiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHLPN
Geng M.M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P., Schneider S., Pohl T., Essig A., Marre R., Melchers K.; "The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                        "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                           STRAIN=AR39
                                                                                                                                                                MEDLINE=20330349; PubMed=10871362; DOI=10.1093/nar/28.12.2311; Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi
                                                                                                                                                                                                                                            Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transferase)
                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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S (in strain: W).
-> ETEA (in strain: W).
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Chlamydiaceae; Chlamydophila.
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of Chlamydia
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BLOCYC; CPNEI15713:CPN0904-MONOMER; -.
BLOCYC; CPNEI18677:CPJ0904-MONOMER; -.
BLOCYC; CPNEI2802:CPB0936-MONOMER; -.
BLOCYC; CPNEI2802:CPB0936-MONOMER; -.
HAMAP; MF_00033; -; 1.
InterPro; IPR007235; Glyco_tran_28_C.
InterPro; IPR004276; Glyco_trans_28_C.
InterPro; IPR004276; Glyco_trans_28_C.
InterPro; IPR004276; Glyco_trans_28_C; 1.
Pfam; PF04101; Glyco_trans_6_C; 1.
Pfam; PF04101; Glyco_trans_6_8; 1.
TIGRFAMS; TIGR01133; murG; T.
Cell cycle; Cell division; Cell shape; Cell wall;
Glycosyltransferase; Inner membrane; Membrane;
                                                                                                                                   Q5SMX2;
21-DBC-2004, integrated into Un:
21-DBC-2004, sequence version 1
21-FBB-2006, entry version 7:
07-FBB-2006, entry version 7:
Basic helix-loop-helix protein-
Name=P049BB01.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE001670; AAD19042.1; -; Genomic DNA.
EMBL; AE002254; AAF38742.1; -; Genomic DNA.
EMBL; BA000008; BAA99112.1; -; Genomic DNA.
EMBL; AE017160; AAP98865.1; ALT_INIT; Genomic DNA.
EMBL; C72022; C72022.
PIR; F86603; F86603.
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22 ORYSA

Q5SMX2 ORYSA

CAMX2;
                                                            namete ετατουστατος (Japonica cultivar-group).
Oryza sativa (Japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Snermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP cla
Spermatophyta; Magnoliophyta; Bhrhartoideae; Oryzeae; Oryza NCBI_TaxID=39947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptidoglycan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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- CATALYTIC ACTIVITY: UDP-N-acetylglucosamine + Mur2Ac(oy)l-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol = UDP + GlCNAc-(l-y4)-Mur2Ac(oyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala)-diphosphoundecaprenol.

- PATHWAY: Peptidoglycan biosynthesis; last step.

SUBCELLULAR LOCATION: Bacterial cell inner membrane; peripheral membrane protein (By similarity)
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; AE001363 GR;
; BA000008 GR;
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Pred. No. 91;
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RESULT 6

Q98L45 RHILO
ID Q98L45;
AC Q98L45;
DT 01-OCT-2001, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2001, sequence version 1.
DT 21-FBB-2006, entry version 22.
DE M111183 protein.
DE M111183 protein.
GN Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rh Phyllobacteriaceae; Mesorhizobium.
OC Bacteria; Proteobacteria; SCALE GENOMIC DNA].
RN RN RN LISHIBABAS SCALE GENOMIC DNA].
RN GI TAXID-381;
RN GI TAXID-381;
RN GI TAXID-3899;
RX MEDLINE=21082930; PubMed=11214968; DOI=10.1093/dn RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato RA Matanabe A., Idesawa K., Ishikawa A., Kawashima K. RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S. RA Takeuchi C., Yamada M., Tabata S.;
RT Token S.; Nakazaki N., Shimpo S. PubM Resorhizobium loti.";
CC Copyrighted by the UniProt Consortium, see http:/
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GO; GO:0030528; F:transcription re
GO; GO:0045449; P:regulation of t:
InterPro; IPR001092; HLH_basic.
InterPro; IPR011598; HLH_DNA_bd.
Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
PROSITE; PS50888; HLH; 1.
SEQUENCE 412 AA; 43709 MW; 644
                                                                                                                                                                            Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bac Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OrderedLocusNames=m111183;
Rhizobium loti (Mesorhizobium loti).
Rhizobium loti (Mesorhizobium loti).
Bacteeria; Proteobacteeria; Alphagroteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP003417; BAD72431.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21082930; PubMed=11214968; DOI=10.1093/dnares/7.6.331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The genome sequence and structure of rice chromosome 1.";
Nature 420:312-316(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22337376; PubMed=12447438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 FSRYAR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FSRYAR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q5SMX2;
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                                      by the UniProt Consortium, see http://www.uniprot.org/terms under the Creative Commons Attribution-NoDerivs License
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulator activity; IEA transcription; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOI=10.1038/nature01184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.1e+02;
thes 0;
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                                                                                                                                                                                                               symbiotic bacterium
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RESULT 7

QSJ1155 AL

QSJ115 AC

QSJ11 AC

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DT 07-I

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Best Local S
Matches 6
Query Match
Best Local Similarity
                                                                     InterPro; IPR003594; ATP_bd_ATPASE.
InterPro; IPR00458; His_kin_like_C.
InterPro; IPR003661; His_kin_A.
InterPro; IPR003667; His_kina_Se.
InterPro; IPR003667; His_kina_Se.
InterPro; IPR00348; Lantibiot_regn.
Pfam; PP00518; HATPASE c; 1.
Pfam; PF00512; HisKA; T.
Pfam; PF00512; HisKA; T.
PF1NTS; PR01784; BCTRLSENSOR.
PRINTS; PR01784; LANTIAEGPROT.
SMART; SM00387; HATPASE c; 1.
SMART; SM00388; HisKA; T.
SMOSITE; PS50109; HIS KIN; 1.
SEQUENCE 432 AA; 48532 MW; 74A8E90.
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GO; GO:0005524; F:ATT binding; IEA.
GO; GO:0003824; F:Cattalyric activity; II
GO; GO:0003866; F:nuclectide binding; II
GO:GO:0000166; F:nuclectide binding; II
InterPro; IPRO11761; ATP GRASP.
PROSITE; PS50975; ATP_GRASP; 1.
ATP-binding; Complete Protecome; Nuclect.
SEQUENCE 427 AA; 46722 MW; F4435AC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=15640200; DOI=10.1128/AEM.71.1.290-296.2005; Wilson M.M., Metcalf W.W.; Wilson M.M., Metcalf W.W.; Oxidation of Reduced Phosphorus Compounds by Alcaligenes faecal:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-FEB-2005, integrated into UniProtKB/TrEMBL. 15-FEB-2005, sequence version 1. 07-FEB-2006, entry version 4.
                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0000155; F:two-component sensor molecule activity; IEA. GO; GO:0006468; P:protein amino acid phosphorylation; IEA. GO; GO:0000160; P:two-component signal transduction system (p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson M., Metcalf W.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=WM2072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=WM207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alcaligenes faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=phoR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q5J1L5_ALCFA
Q5J1L5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; GO:0016020; (
; GO:0005524; I
; GO:0016301; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AY548383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:ATP binding; IEA. F:kinase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58
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C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alcaligenes
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46722 MW; F4435ACIEDC7F645 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 1.
  Score 31;
Pred. No.
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                                                                             74A8E901880BF476 CRC64;
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                          DB 2;
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                       Length 432;
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                                              Q45AY3 9BURK PRELIMINARY; PRT; 460 Q45AY3; 13-SEP-2005, integrated into UniProtKB/T 13-SEP-2005, sequence version 1. 07-FEB-2006, entry version 5. Amino acid permease-associated region. ORFNames=BcenDRAFT 5191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E., Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F., Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S., Selengut J., Shamblin C., Radune D., Romero C.M., Sarria R., Zhou L., Fraser C.M., Sullivan S.A., White O., Y "Structural flexibility in the Burkholderia mallei genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006279; F:amino acid-polyamine transporter
GO; GO:0006865; P:amino acid transport; IEA.
GO; GO:00068610; P:transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR002293; AA/rel_permease.
InterPro; IPR004841; Permease_region.
PANTHER; PTHR1785; AA/rel_permease1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q62CX5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 23344;
PubMed=15377793; DOI=10.1073/pnas.0403306101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burkholderia mallei (Pseudomonas mallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2004,
25-OCT-2004,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00324; AA_permease; 1.
PROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid permease
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                                Burkholderia
                                                                                                                                                                                                                                           9
9BURK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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BMAA0717;
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447 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                           cenocepacia AU 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 integrated into UniProtKB/TrEMBL sequence version 1.
                                                                                                                                                                 integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
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     Betaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A209ED83F6C1D427 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic_DNA.
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thes 0;
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        Burkholderiales;
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RESULT 10
Q4LTZ2_9BURK
ID Q4LTZ2_9BURK
AC Q4LTZ2;
AUG-2005, s
DT 02-AUG-2005, s
DT 07-FEB-2006, e
DE Amino acid per
GN ORFNames=Bcen2
OS Burkholderiac
OC Burkholderiac;
OC Burkholderiac;
OC Burkholderiac;
OX NCBI_TaxID=33
RP NUCLEOTIDE SEC
RC STRAIN=HI2424,
RG US DOE Joint G
RA Copeland A., I
RA Hammon N., Iss
RT HI2424.";
RL Submitted (JUN
RN [2]
RP NUCLEOTIDE SEC
RT SUBMITTED SEC
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00324; AA permease; 1.

Pfam; PF00324; AA permease; 1.

PROSITE; PS00218; AMINO ACID PERMEASE 1; 1.

PROSITE; PS00218; AMINO ACID PERMEASE 1; 1.

SEQUENCE 460 AA; 49648 MW; 68780B9E9F03369D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K.,
Hammon N., Israni S., Pitluck S., Richardson
"Sequencing of the draft genome assembly of E
AU 1054.";
STRAIN=HI2424;
US DOE Joint G
                                                                                                                                   Copeland A., Lucas S., Lapidus A., Barry K., Hammon N., Israni S., Pitluck S., Richardson "Sequencing of the draft genome assembly of HI2424.";
                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                                                                                                                                                                                                                                                                                                                                                                             Burkholderia cenocepacia HI2424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid permease-associated region. ORFNames=Bcen2424DRAFT_4131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-2005, sequence version 07-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-AUG-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU 1054.
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NCBI_TaxID=331271;
                                                                                                                                                                                                                                           US DOE Joint Genome Institute (JGI-PGF);
                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=331272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Larimer F., Land M.; "Annotation of the draft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=AU
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                                                         NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002293; AA/rel_permease1
InterPro; IPR004840; AAc_permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0016021; C:integral to membrane; GO:0016020; C:membrane; IEA.
GO:0005279; F:amino acid transport; GO:0006865; P:amino acid transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0006810;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAHI01000004; EAM13792.1; -;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assembly of Burkholderia
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rane; IEA.
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P.;
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Q395V1_BURS3
Q395V1;
22-NOV-2005,
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GO; GO:00
GO; GO:00
COmplete
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GO; GO:0006810; P:transport; IEA.
InterPro; IPR00223; AA/rel_permease1.
InterPro; IPR004840; AAc_permease.
PANTHER; PTHR11785; AA/rel_permease1; 1.
Pfam; PF00324; AA permease; 1.
PROSITE; PS00218; AMINO ACID PERMEASE 1; 1.
SEQUENCE 460 AA; 49648 MW; 68780B9E9F03369D
                                                                                                                                                                                                                                                                                                                                                                                                                 Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T., Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M., Vergez L., Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid transporter.
OrderedLocusNames=Bcep18194_B1646;
Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            888
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                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                     "Complete sequence of chromosome 2 of Burkhold Submitted (OCT-2005) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
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                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=269483;
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                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC
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Local Similarity
les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOE
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GO:0016020; C:membrane; IEA.
GO:0005279; F:amino acid-polyamine transporter
                                                                                                                                L; CP000152; ABB11760.1; -; Genomic_DNA.
G0:0016021; C:integral to membrane; IEA.
G0:0016020; C:membrane; IEA.
G0:0005279; F:amino acid-polyamine transporter
G0:0006865; P:amino acid transport; IEA.
G0:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Joint Genome Institute;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 6; Conserv
                                                                                       proteome.
460 AA;
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Pred. No. 1.2
); Mismatches
                     Score 31; DB 2;
Pred. No. 1.2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                          D6BBAA9AF2CD5155 CRC64;
  Mismatches
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1.2e+02;
thes 0;
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                                                                                                                                                                                                                                                                                                                                                                          databases.
                                           Length 460;
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                                                                                                                                                                                    activity; IEA.
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Q3JFR3 BURP1
Q3JFR3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Palmer N., Dodson R.,
Hickey B.K., Gwinn M., Dougherty B., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van-Vugt R., Adams M.D., Gocayne J.D., Weidman J., Utterback T.,
Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C.,
Cotton M.D., Horst K., Tomb J.-F., Roberts K., Hatch B., Smith H.O.,
Venter J.C.;
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                              EMBL;
TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid permease.
ORFNames=BTH_II1560;
Burkholderia thailandensis
   8888
                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
Woods D.E., Nierman W.C.;
Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-NOV-2005, integrated into UniProtKB/TrEMBL 08-NOV-2005, sequence version 1. 21-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/toDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=320372;
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Q2T4Z4;
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BURTH
L; CP000125; ABA52590.1; -; Genomic_DNA.
R; BURPS1710b_A2440; -.
GO:0016021; C:integral to membrane; IEA.
GO:0016020; C:membrane; IEA.
GO:0005279; F:amino acid-polyamine transporter
GO:0006865; P:amino acid transport; IEA.
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NCE 461 AA; 49957 MW; 7F1195E772F28B65
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PROSITE; PS00218; AMINO_ACID_PERMEASE_1;
Complete proteome.
SEQUENCE 461 AA; 50051 MW: 20021177.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L., Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R., Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I., Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D., Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K., Keith K.E., Maddison M., Moule S., Price C., Quail M.A., Keith K.E., Matcherford K., Sanders M., Simmonds M., Sanders M., Simmonds M., Sanders M., Simmonds M.,
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25-OCT-2004, sequence version 1.
07-FEB-2006, entry version 17.
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InterPro; IPR002293; AA/rel_permease1
InterPro; IPR004840; AAc_permease.
InterPro; IPR004841; Permease_region.
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
GO; GO:0006865; P:amino acid transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR004840; AAC permease.
InterPro; IPR004840; AAC permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burkholderia pseudomallei.";
Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=proY; OrderedLocusNames=BPSS0845;
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PROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whitehead S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=15377794;
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RA Azevedo V. Bertero M.G., Beesieres P., Bolotin A. Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.-K., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T.,
RA Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T.,
RA Chi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Gliseppi G., Guy B.J., Haga K., Halech J. Harwood C.R., Henaut A.,
RA Gliseppi G., Guy B.J., Haga K., Halech J., Klaerr-Blanchard M.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,
Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Redigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Robeck M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Raeger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadaie Y., Sato T., Sekowska A., Seror S.J., Serror P.,
RA Rose M., Sadaie Y., Sato T., Sekowska A., Seror S.J., Serror P.,
RA Rose M., Sadaie Y., Sato T., Sekowska A., Seror S.J., Serror P.,
RA Rose M., Sadaie Y., Viari A., Wambutt R., Wedler E., Wedler F.,
RA Wassarotti A., Wambutt R., Wedler E., Wedler F.,
RA Yoshikawa H., Danchin A., Tanaka H.-F., Zumstein E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998, integrated into UniProtKB/TrEMBL 01-JAN-1998, sequence version 1. 07-FEB-2006, entry version 30. Amino acid transporter (YtnA protein). Name=ytnA; OrderedLocusNames=BSU30530; Bacillus subtilis.
EMBL; Z99119; CAB15031.1; -; Geno PIR; C69997; C69997, C69997, C69997, Go; GO:0016021; C:integral to mem GO; GO:0016021; C:membrane; IBA. GO; GO:0005279; F:amino acid-poly
                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/toustributed under the Creative Commons Attribution-NoDerivs License
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Submitted (JUN-1997)
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NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
CORONARA 67; PubMed=9387221;
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034618; Q795P5;
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Yoshikawa H., Danchin A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Yoshikawa H., Danchir
"The complete genome
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   acid-polyamine transporter activity; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sorokin
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                                                                                                                                                                      Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                 of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                    Genomic_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Α.,
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n of the
                                                                                                                                                                      DNA
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                                                                                                                                                                                                 DNA.
                                                                                                                                                                                                                                                                                                   see http://www.uniprot.org/terms
                                                                       IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
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RESULT 16
Q2STX5 BURN
ID Q2STX
AC Q2STX
AC Q2STX
AC Q2STX
DT 24-JI
DT 07-FI
DT 07-FI
DT 07-FI
DT 07-FI
DT 07-FI
ROUTH
OS BUTK
OC BUTK
OC BUTK
OX NCBI
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RN (1)
RN (1)
RN (1)
RN (2)
RESULT 17
Q3JY99 BURP1
ID Q3JY99;
AC Q3JY99;
DT 08-NOV-2005, 107
21-FEB-2006, 107
CM orderediocusNa.
OS Burkholderia;
OC Bacteria; Proto
OC Burkholderiace
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Palmer N., Dodson R.,
Hickey E.K., Gwinn M., Dougherty B., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van-Vugt R., Adams M.D., Gocayne J.D., Weidman J., Utterback T.,
Watthey L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C.,
Cotton M.D., Horst K., Tomb J.-F., Roberts K., Hatch B., Smith H.O.,
Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid permease.
ORFNames=BTH_I3129;
Burkholderia thailandensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0006865; P:amino acid transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR002293; AA/rel_permease1.
InterPro; IPR004840; AAc_permease.
InterPro; IPR004841; Permease_region.
PANTIER; PTHR11785; AA/rel_permease1; 1.
Burkholderia pseudomallei (strain 1710b).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; pseudomallei group.
                                                                                                                                08-NOV-2005, integrated into UniProtKB/TrEMBL 08-NOV-2005, sequence version 1. 21-FEB-2006, entry version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; pseudomallei group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JAN-2006, sequence version 07-FEB-2006, entry version 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00324; AA_permease; 1.
PROSITE; PS00218; AMINO_ACID_PERMEASE_1;
                                                                               Amino acid permease.
OrderedLocusNames=BURPS1710b_0036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=271848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JAN-2006,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CP000086; ABC38752.1;
NCE 468 AA; 50779 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76
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463 AA; 50328 MW; B21F9F40AB1C7180 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       FSRYAR 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 2; 1
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic DNA.
A905AA5CB57B7284 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Best Local
                                              GO; GO:0016021; GG; GO:0016020; GG; GO:0005279; GG; GO:0006865; FG; GO; GO:0006810; FR0022
                                                                                                                                                                                                                                                                                                                                                     Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E., Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E., Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson Durkin A.S., Gwinn M.L., Haff D.H., Khouri H.M., Kolonay J.F., Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Y Zafar N., Zhou L., Fraser C.M., Zhou L., Fraser C.M., "Structural flexibility in the Burkholderia mallei genome."; "Structural flexibility in the Burkholderia mallei genome.";
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:inembrane; IEA.

GO; GO:0016020; C:inembrane; IEA.

GO; GO:0005279; F:amino acid-polyamine transporter activity;

GO; GO:000685; P:amino acid transport; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR002293; AA/rel_permease1.

InterPro; IPR004294; AAc permease

InterPro; IPR004294; Permease region.

Pfam; PF00324; AA permease; 1.

PROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004, integrated into 0
25-OCT-2004, sequence version
07-FEB-2006, entry version 16
                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/teDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=15377793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Betar
Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burkholderia mallei (Pseudomonas mallei).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid permease.
OrderedLocusNames=BMA2796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q62G62;
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                                                                                                                                                                                                           TIGR;
                                                                                                                                                                                                                                   EMBL;
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                             interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18
BURMA
          BMA2796;
C:integral to membrane; IEA.
0:0016021; C:integral to membrane; IEA.
0:0016020; C:membrane; IEA.
0:0005279; F:amino acid-polyamine transporter.
0:0006865; P:amino acid transport; IEA.
0:0006810; P:transport; IEA.
0:pro; IPR002293; AA/rel_permease1.
Pro; IPR004894; AAC_permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TaxID=13373;
                                                                                                                                                                                                                                   CP000010; AAU47957.1; -;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE [LARGE SCALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOI=10.1073/pnas.0403306101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50889 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Betaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB
Pred. No. 1.2
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EBEFA2C3CE681110
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                                                                                                                                                                                                                                                                                                               see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
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                                                                                                                                 activity;
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RESULT 19
Q63PW6_BURPS
ID Q63PW6_COT-2004, s
AC Q63PW6;
AC Q7-2004, s
DT 25-CCT-2004, s
DT 25
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                                                                                                            Query Match
Best Local S
Matches 6
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L., Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R., Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I., Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D., Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K., Keith K.E., Maddison M., Moule S., Price C., Quail M.A., Keith K.E., Maddison M., Sanders M., Simmonds M., Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M., Shitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J., "Genomic plasticity of the causative agent of melioidosis, Burkholderia bseudomallei":
                                                                                                                                                                                                                                            Pfam; PF00324; AA Dermease; 1.
PROSITE; PS00218; AMINO_ACID_PERMEASE_1;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BX571965; CAH37269.1; -; Genomic_DNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
GO; GO:0006865; P:amino acid transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR002293; AA/rel permeasel.
InterPro; IPR004840; AAC_permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           063PW6;
25-OCT-2004, integrated into Ur
25-OCT-2004, sequence version 1
07-FEB-2006, entry version 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PANTHER; PTHR11785; AA/rel_permease1; 1.
Pfam; PF00324; AA permease; 1.
PROSITE; PS00218; AMINO_ACID_PERMEASE_1;
Complete proteome.
SEQUENCE 468 AA; 50949 MW; AAEEB96964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Holden M.T.G., Titball R.W., Peacoc
Atkins T., Crossman L.C., Pitt T.,
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004841; Permease_region.
PANTHER; PTHR11785; AA/rel_permease1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burkholderia pseudomallei.";
Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=15377794; DOI=10.1073/pnas.0403302101; Holden M.T.G., Titball R.W., Peacock S.J., Ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=K96243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; pseudomallei group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burkholderia pseudomallei (Pseudomonas pseudomallei)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OrderedLocusNames=BPSL3256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=28450;
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mes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78
  78
                                                                                                            Similarity 6; Conser
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                                                       FSRYAR
  FSRYAR
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                                                                                                                                                                                                                           468
                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                           AA,
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                                                                                                                                                                                                                           50875 MW;
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                                                                                                                                      100.0%;
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Pred. No.
                                                                                                                                   Score 31; DB 2;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                           69E6B0D62E681105 CRC64;
                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                Length 468;
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RESULT 20

ANCH PROVIDE AND ANCH PROVIDED TO 11-NOV DT 01-NOV DT 0
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                                                        Query Match
Best Local S
Matches 6
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HSSP; P11546; IPBG.
GenomeReviews; U00096 GR; b2716.
EchoBASE; EB0083; -. 
EcoGene; EG10085; ascB.
BioCyc, EcoCyc.EG10085-MONOMER; -.
R InterPro; IPR001360; Glyco_hydro_1.
R PANTHER; PTHR10353; Glyco_hydro_1; 1.
                                                                                                                                                        CONFLICT
SEQUENCE
                                                                                                                                                                                                      ACT_SITE
ACT_SITE
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Nucleotide sequence, function, activation, cryptic asc operon of Escherichia coli K12.' [9]. Biol. Evol. 9:688-706(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997, sequence version 2. 07-MAR-2006, entry version 51. 6-phospho-beta-glucosidase ascB (EC Name=ascB; OrderedLocusNames=b2716;
                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
Complete proteome; Glycosidase; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00232; Glyco_hydro_1
PRINTS; PR00131; GLHYDRLASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M73326; AAA16430.1; -; Unassigned_DNA.
EMBL; U29579; AAA69226.1; ALT INIT; Genomic_DNA.
EMBL; U2096; AAC75758.1; -; Genomic_DNA.
PIR; H65051; H65051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mau B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE
STRAIN=K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P24240; P78104; Q59375; 01-MAR-1992, integrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H(2)0 = D-glucose + D-glucose 6-phosphate.
-i- SIMILARITY: Belongs to the glycosyl hydrolase 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Can hydrolyze salicin, cellobiose, and probably arbutin.
-!- CATALYTIC ACTIVITY: 6-phospho-beta-D-glucosyl-(1,4)-D-glucose +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hall B.G., Xu L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92334140; PubMed=1630307;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997)
                                                      Similarity6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shao Y.;
FSRYAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE [LARGE / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                           Conservative
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/FTId=PRO 0000063895.
Proton domor (Potential).
Nucleophile (By similarity).
EA -> GT (in Ref. 1).
                                                                                Score 31; I
Pred. No. 1
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S -> C (in Ref.
RK -> HR (in Ref
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RESULT 22
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Best Local Similarity
""" hes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6-phospho-beta-glucosidase.

Name=ascB; OrdereduccusNames=SDY 2912;

Shigella dysenteriae serotype 1 (strain Sd197).

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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06-DEC-2005, sequence version
                                                                                                                                                                                                                 Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Qiang B., Hou Y., Yu J., Jin Q., "Genome dynamics and diversity of Shigella species, the agents of bacillary dysentery.";

Nucleic Acids Res. 33:6445-6458(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-2005, integrated into UniProtKB/TrEMBL 06-DEC-2005, sequence version 1. 07-FEB-2006, entry version 4.
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                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=16275786; DOI=10.1093/nar/gki954;
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                               GO; GO:0004553;
GO; GO:0005975;
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl
GO:0005975; P:carbohydrate metabolism; IEA.
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                                                         CP000034; ABB62941.1; -; Genomic_DNA.
D:0004553; F:hydrolase activity, hydrolyzing O-glycosyl
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                                  metabolism;
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L., Chen S.,
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PubMed=16275786; DOI=10.1093/nar/gki954;

Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,

Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.

Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,

Qiang B., Hou Y., Yu J., Jin Q.;

"Genome dynamics and diversity of Shigella species, the etiologic agents of bacillary dysentery.";

Nucleic Acids Res. 33:6445-6458(2005).
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38 SHISS
38 SHISS
Q3YYEB SHISS PRELIMINARY; PRT; 474 AA.
Q3YYEB;
Q3YYEB;
integrated into UniProtKB/TrEMBL
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21-FEB-2006, integrated into UniProtKB/TrEMBL
21-FEB-2006, sequence version 1.
07-MAR-2006, entry version 2.
Cryptic 6-phospho-beta-glucosidase.
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07-FEB-2006, entry version 5.
6-phospho-beta-glucosidase, cryptic.
Name=ascB; OrderedLocusNames=SSO_2860;
Shigella sonnei (strain Ss046).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00131; GLHYDRLASE1.

PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1;

PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2;
                                                                                              Bacteria; Proteobacteria;
                                                                                                                        Escherichia coli W3110.
                                                                                                                                                  Name=ascB
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                                           NCBI_TaxID=316407;
                                                                          Enterobacteriaceae;
  NUCLEOTIDE SEQUENCE
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                                                                                              Gammaproteobacteria;
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Pred. No. 1.2e+02;
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RESULT 25

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PRELIMINARY; PRT; 474 AA.

AC Q8X841; Q7ABC1;

DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.

DT 01-MAR-2002, sequence version 1.

DT 07-FEB-2006, entry version 26.

DE 6-phospho-beta-glucosidase; cryptic (6-phospho-be

Name-ascB; OrderedLocusNames=EC3572, z4024;

OS Escherichia coli 0157:H7.

OC Bacteria; Proteobacteria; Gammaproteobacteria; En

Bacteria; Proteobacteria; Gammaproteobacteria; En

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=83334;

RN UCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;

RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35

RA Perna N.T., Plunkett G. III, Burland V., Mau B.,

RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Ki

RA Posfai G., Hackett J., Klink S., Boutin A., Shao

RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Sc
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STRAIN=K-12;
STRAIN==93094132; PubMed=1459951;
MEDLINE=93094132; PubMed=1459951;
Gervais F.G., Drapeau G.R.;
Gervais F.G., Cloning, and characterization of rcsF, a new
""" Annification, cloning, and characterization of rcsF, a new
""" exopolysaccharide synthesis that suppresses
""" herichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Rhs
                                                                                                                                                                                                                                                                                                                            6-phospho-beta-glucosidase; cryptic (6-phospho-
Name-ascB; OrderedLocusNames=EC63572, z4024;
Escherichia coli 00157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN-0157:H7 / EDL933 / ATCC 700927 / HEIG.
MEDLINE-21074935; PubMed-11205651; DOI=10.1038/35054089;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Posfai G., Hackett J., Klink S., Boutinn A., Shao Y., Miller L.,
Posfai G., Hackett J., Klink S., Boutinn A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Link A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
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"Structural requirements for the proving the standard of the proving the standard of the proving the standard of th
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-2005, sequence version 1.
21-FEB-2006, entry version 4.
Permease for cytosine/purines, uracil,
OrderedLocusNames=Pfl_3440;
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BioCyc; BCOLB334-1:ECS3572-MONOMER; -. hydrolyzing GO; GO:0004553; F:hydrolase activity, hydrolyzing GO; GO:0005975; P:carbohydrate metabolism; IEA. InterPro; IPR001360; GJyco_hydro_1.
PANTHER; PTHR10135; GJyco_hydro_1; 1.
Pfam; PF00232; Glyco_hydro_1; 1.
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Copeland A., Lucas S.,
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PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1;
PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2;
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  L; CP000094; ABA75178.1; -; Genomic_DNA.
GO:0016020; C:membrane; IEA.
GO:0015205; F:nucleobase transporter activity;
GO:0015931; P:nucleobase, nucleoside, nucleotic
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Q2X8L3;
10-JAN-2006,
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Pseudomonas putida (strar.
Bacteria; Proteobacteria;
                                        01-JUN-2003, sequence version 1.
07-FEB-2006, entry version 10.
Transporter, NCS1 nucleoside transporter family.
OrderedLocusNames=PP4035; ORENames=PP 4035;
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Larimer F., Land M.;
"Annotation of the draft genome assembly of Pseudomonas |
Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w
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Pseudomonas putida F1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;

MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou l Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;

Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
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Q91674;
Q91674;
Q1-MAR-2001, integrated into UniProtKB/TrEMBL.
Q1-MAR-2001, sequence version 1.
Q7-FEB-2006, entry version 15.
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Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martine dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherry S.C., Kolonay J.F.
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.
Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence and comparative a metabolically versatile Pseudomonas putida Environ. Microbiol. 4:799-808(2002).
                    EMBL;
                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                           "Complete genome sequence of Pseudomonas aeruginosa opportunistic pathogen.";
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NCBI_TaxID=160488;
                                                                                                                                                                       Nature 406:959-964(2000).
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GO:0015205; F:nucleobase transporter activity; IEGO:0015931; P:nucleobase, nucleoside, nucleotide
: AE004481; AAG03832.1;
B83591; B83591.
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RESULT 31
Q8PQL8 XANAC
ID GPQL8 X
AC Q8PQL8;
DT 01-OCT-2
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W8 XANC5
Q3BYW8 XANC5
Q3BYW8;
22-NOV-2005, 1
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PubMed=16237009; DOI=10.1128/JB.187.21.7254-7266.2005;

PubMed=16237009; DOI=10.1128/JB.187.21.7254-7266.2005;

Thieme F., Koebnik R., Bekel T., Berger C., Boch J., Buettner C., Caigalat L., Goesmann A., Kay S., Kirchner O., La Linke B., McHardy A.C., Meyer F., Mittenhuber G., Nies D.H., Niesbach-Kloesgen U., Patschkowski T., Rueckert C., Rupp O., Schneiker S., Schuster S.C., Vorhoelter F.J., Weber E., Puehl Bonas U., Bartels D., Kaiser O.;

"Insights into genome plasticity and pathogenic Bacterium Kanthomonas campestris pv. vesicatoria restrictions of the plastic bacterium Kanthomonas campestris pv. vesicatoria restrictions."
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0015205; F:nucleobase transporter activity; IEA.
GO; GO:0015331; P:nucleobase, nucleoside, nucleotide and nucl.
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07-FEB-2006,
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                                                    01-OCT-2002, integrated into t
01-OCT-2002, sequence version
07-FEB-2006, entry version 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AM039952; CAJ21945.1; -; Genomic DNA.
GG; GO:0008415; F:acyltransferase activity; IEA.
GO; GO:0003840; F:gamma-glutamyltransferase activity;
GO; GO:0016740; F:transferase activity; IEA.
Acyltransferase; Complete proteome; Transferase.
SEQUENCE 526 AA; 55499 MW; B40B3B743818AA43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by the complete genome sequence."; J. Bacteriol. 187:7254-7266(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xanthomonas campestris pv. vesicatoria (strain 85-10).
Bacteria, Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=ggt1; OrderedLocusNames=XCV0314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gamma-glutamyltranspeptidase (EC 2.3.2.2).
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Pfam; PF02133; Transp_cyt_pur; 1.
                           Gamma-glutamyltranspeptidase
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RA Camargo I.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F.,
RA Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
RA El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,
RA El-Dorry M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menok C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Moreira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
T. Grannarison of the genome.
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STRAIN-74-OR33-1A / FGSC 987;

MEDLINE-22598136; PubMed=12712197; DOI=10.1038/nature01554;
Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L., Smirnov S., Purcel U., Rehman H Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A., Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-2003, integrated into UniProtKB/TrEMBL 15-DEC-2003, sequence version 1. 07-FEB-2006, entry version 11. Hypothetical protein. ORFNames=NCU07334.1;
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Bacteria; Proteobacteria; Gamm
Xanthomonadaceae; Xanthomonas.
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GO; GO:0003840; F:gamma-glutamyltransferase
GO; GO:0003840; F:gamma-glutamyltransferase
InterPro; IPR000101; GGT_peptidase;
PANMHER; PTHR11686; GGT_peptidase; 1.
Pfam; PF01019; G_glu transpept; 1.
PRINTS; PR01210; GGTRANSPTASE.
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                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; P
Sordariomycetidae; Sordariales;
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SEQUENCE 526 AA;
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                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE
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                                                                                                                                                                                                                                                                                 Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., G Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Sh Vergez L., Schmuz J., Larimer F., Land M., Hauser L., Pell Kyrpides N., Anderson I., Oda Y., Harwood C.S., Richardson "Complete sequence of Rhodopseudomonas palustris HaA2."; Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
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07-MAR-2006, sequence version 1.
07-MAR-2006, entry version 1
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GO; GO:0015205; F:nucleobase transport
GO; GO:001591; P:nucleobase, nucleosi
InterPro; IPR001248; Cyt_pur_permease.
InterPro; IPR012681; NCS1.
Pfam; PF02133; Transp_cyt_pur; 1.
TIGRFAMs; TIGR00800; ncs1; 1.
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NCBI_TaxID=316058;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome sequence of the filamentous fungus Neurospora crassa.", Nature 422 \colon 859 - 868 \ (2003) .
                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria;
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                                                                                SEQUENCE
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O:0016020; C:membrane; IEA.
O:0015205; F:nucleobase transporter activity; IEA.
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Q374J7;
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SIGNAL
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19-JUL-2005, sequence version 1
07-FEB-2006, entry version 6
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Larimer F., Land M.;
"Annotation of the draft genome of Rhodop:
BisA53.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copeland A., Lucas S., Lapidus A., Barry K., Hammon N., Israni S., Pitluck S., Richardson "Sequencing of the draft genome and assembly palustris BisA53.";
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                           Tetraodon nigroviridis
Eukaryota; Metazoa; Chc
                                                                                   (Fragment).
ORFNames=GSTENG00020461001;
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                                                                                                                                                       Chromosome undetermined
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BisA53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BisA53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE
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peland A., Lucas S., Lapidus A., Barry K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAUTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO:0005215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAUTION: The sequence sh
EMBL/GenBank/DDBJ whole
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                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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74262 MW;
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n puffer).
; Craniata;
Teleostei;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8e+02;
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   Vertebrata;
Euteleostei;
                                                                                                                                                    genome
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of Rhodopseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detter J.C.,
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                                                                                                                                                    shotgun
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                                  Euteleostomi;
                                                                                                                                                       sequence
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RESULT 36
Q4P6R1 USTWA
ID Q4P6R1 U
AC Q4P6R1 T
DT 19-UUL-2
DT 19-UUL-2
DT 19-UUL-2
DT 07-FEB-2
DE Hypothet
GN ORFNames
OS Ustilagi
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RN [1]
RP NUCLEOTI
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RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Micaud S., Jaffe D., Fishers S., Lutfalla G., Dossat C., Segurens B.,

RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

RA Anthouard V., Jubin C., Castelli V., Roulain J., De Berardinis V.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,

RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals

"T the early vertebrate proto-karyotype.";

Lander 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                              Q4P6R1_USTMA PRELIMINARY;
Q4P6R1;
19-JUL-2005, integrated into U
19-JUL-2005, sequence version
07-FEB-2006, entry version 4.
                                                                                                                                 Hypothetical protein.
ORFNames=UM04202.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope; Whitehead Institus Submitted (FEB-2004) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
TCBI_TaxID=99883;
                                                                          Eukaryota; Fungi; Basidiomycota; Us
Ustilaginomycetidae; Ustilaginales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01013; OSBP; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01237; Oxysterol B
PRINTS; PR00360; C2DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE
                                                                                                                 Ustilago maydis 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000008; C2.
InterPro; IPR000648; Oxysterol_bd
InterPro; IPR001849; PH.
                     NUCLEOTIDE
                                                      NCBI_TaxID=237631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L; CAAE01014653; CAG01633.1; -; Genomic D
GO:0003676; F:nucleic acid binding; IEA.
GO:0006869; P:lipid transport; IEA.
GO:0008202; P:steroid metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAUTION: The sequence shown here is derived EMBL/GenBank/DDBJ whole genome shotgun (WGS)
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                                                                                                                                                                                                                                                                                                                                         742
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ER 809 809
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                                                                                                                                                                                                                                                                                                                                         FSRYAR 747
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                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                        integrated into UniProtKB/TrEMBL
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                     [LARGE
                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 31; DB 2; 100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Institute Centre for Genome Research; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                     SCALE
                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3199F0A349871EB4 CRC64;
                     GENOMIC
                                                                        Ustilaginomycetes;
es; Ustilaginaceae; Ustilago.
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                                                                                                                                   Matches
                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006035; Arg_agm_form.
InterPro; IPR006615; Pept C19 N 1.
InterPro; IPR001394; PeptIdase_C19.
Pfam; PF00443; UCH; 1.
SMART; SM00695; DUSP; 1.
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                                                                                                                                                                                                                                                                                                                        PROSITE; PS00147; ARGINASE 1; PROSITE; PS00972; UCH 2 1; 1. PROSITE; PS00973; UCH 2 2; 1. PROSITE; PS50225; UCH 2 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The genome sequence of Ustilago maydis.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                   Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0004197; F:cysteine-type endopeptidase activity; GO; GO:0004221; F:ubiquitin thiolestrase activity; IEA GO; GO:0006512; P:ubiquitin cycle; IEA GO; GO:0006512; P:ubiquitin cycle; IEA GO; GO:0006511; P:ubiquitin-dependent protein catabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Distributed under the Creative Commons Attribution-NoDerivs License
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896 FSRYAR 901
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1427 AA;
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                                                                                                                                                                   Score 31; DB 2;
Pred. No. 4e+02;
                                                                                                                                   Mismatches
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RESULT 37
Q57UM9 9TRYP
ID 057UM9;
O57UM9;
O57UM9;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 10-MAY-2006, entry version 3.
DE Mitochondrial DNA polymerase I protein C.
GN ORFNames=Tb927.7.3990;
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanoson OX NCBL_TaxID=5691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
STRAIN-GUTATL10.1;
RA Shallom J., Hou L., Djikeng A., Feldblyum T., Hos Shallom J., Jones K., Koo H.L., Larkin C., Pai GRA Johnson J., Jones K., Koo H.L., Larkin C., Pai GRA Johnson J., Jones K., Koo H.L., Fraser C.M., El Submitted (APR-2005) to the EMBL/GenBank/DDBJ dat C.
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DR GO: GO:000387; F:DNA-directed DNA polymerase act GO; GO:000387; F:DNA-directed DNA polymerase act GO; GO:0006280; P:DNA-binding; IEA.
DR GO; GO:0006280; P:DNA-poll.
DR FINTS; PR00868; DNA-POLI.
DR PRINTS; PR00868; DNA-POLI.
DR PRINTS; PR00868; DNA-POLI.
SQ SEQUENCE 1649 AA; 182029 MW; "2FC694772CCZA7AII
QBMWB JYR
ID QBMWB
AC QBMWB
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DT 01-OC
DT 01-FE
DR NA F
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GO; GO:0003887; F:DNA-directed DNA polymerase activity; GO; GO:0006260; F:DNA replication; IEA.
InterPro; IPR001998; DNA pol.
InterPro; IPR002298; DNA pol.
Pfam; PF00476; DNA pol A; 1.
PRINTS; PR00868; DNAPOLI.
PROSITE; PS00447; DNA POLYMERASE A; UNKNOWN 1.
PROSITE; PS00447; DNA POLYMERASE A; UNKNOWN 1.
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01-OCT-2002, sequence version 1.
07-FEB-2006, entry version 15.
DNA polymerase I-like protein C.
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                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                             MEDLINE=22146561; PubMed=12150917; DOI=10.1016/S1097-2765(02)00571-3; Klingbeil M.M., Motyka S.A., Englund P.T.; "Multiple mitochondrial DNA polymerases in Trypanosoma brucei."; Mol. Cell 10:175-186(2002).
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Q8MWB3_9TRYP
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                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trypanosoma brucei.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=TREU927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                    L; AF445378; AAM81964.1; -; Genomic_DNA. GG:0003677; F:DNA binding; IEA. GO:0003867; F:DNA-directed DNA polymerase GO:0005260; P:DNA replication; IEA.
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_TaxID=5691;
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   IPR001098;
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                 27 9CAUD PRELIMINARY; PRT; 102 AA. 056EC7; 9CAUD PRELIMINARY; PRT; 102 AA. 056EC7; 10-MAY-2005, integrated into UniProtKB/TrEMBL. 10-MAY-2005, sequence version 1. 07-FEB-2006, entry version 2. Hypothetical protein PHG310RF237C. Hypothetical protein PHG310RF237C. Name=PHG310RF237C; ORFNames=PHG31p234;
                                                                                                                                                                                                                                          EMBL; D;
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Ffam; PF00476; DNA pol A; 1.

PRINTS; PR00868; DNAPOLL.

PROSITE; PS00447; DNA POLLYMERASE A; UNKNOWN 1.

SEQUENCE 1649 AA; 182043 MW; DAABC43C737A3BB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sano K., Miyata M.;
"The gyrB gene lies opposite from circular chromosome of Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996,
01-NOV-1996,
                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                           Distributed under the Creative Commons Attribution-NoDerivs
                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium,
                                                                                                                                                                                                                                                                                                           Submitted (NOV-1993) to the
                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC27343;
Sano K., Miyata M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC27343;
MEDLINE=95129856; PubMed=7828871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA gyrase subunit A (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996, sequence version 07-FEB-2006, entry version 23.
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 Viruses; dsDNA viruses,
            Aeromonas phage
                                                                                                                                                                                                                                                                                                                       Sano K.-1
                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC27343;
                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-1994)
                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 151:181-183(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma capricolum
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_MYCCA
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 RNA stage; Caudovirales; Myoviridae
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                     AMEDILIBE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McGwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q5U3N8_BRARE PRELIMINARY; PRT; 110 AA. Q5U3N8; Q7-DEC-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                Director MGC F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                Copyrighted
Distributed
                                                                                                                                                                                                 Director MGC Project;
Submitted (NOV-2004) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Larvae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=wrb;
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                             Ensembl;
                                                        EMBL;
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                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE
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BRARE
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                                                        BC085456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
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5; Conserv
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                             ENSDARG00000024641; Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aı protein.
102 AA; 1
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                                                        AAH85456.1; -;
                                                                                                                                           UniProt
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83.3%;
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                                                                                                                                           Consortium,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Craniata;
Teleostei;
                                                                                                                                                                                                                                                                                                                                         99:16899-16903 (2002)
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Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniform
                                                        mRNA.
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                                rerio
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                                                                                                                see http://www.uniprot.org/terms
Attribution-NoDerivs License
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hage 31 genome.";
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RESULT ID SOULT OF SO
RESULT 43
Q3JQBB E BURP1
ID Q3JQBB;
AC Q3JQBB;
DT 08-NOV--
DT 08-NOV--
DT 21-FEB--
DB Hypothee
GN Ordered
OC Bacterial
OC Bacterial
OC Burkhol
OC Burkhol
OC Burkhol
RN NUCLEOTI
RA Woods D.
RL Submitte
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                                                                                                                                          OUBB BURF1 PRELIMINARY; FRI; OJJOBB BURP1 PRELIMINARY; FRI; OJJOBB;

1 QJJQBB;

1 08-NOV-2005, integrated into UniProtKB/TrEMBL.

1 08-NOV-2005, sequence version 1.

21-FEB-2006, entry version 4.

1 21-FEB-2006, entry version 4.

21-FEB-2006 sequence version 1.

21-FEB-2006 entry version 4.

21-FEB-2006 entry version 4.

21-FEB-2006 sequence version 1.

21-FEB-2006 entry version 4.

21-FEB-2006 entry version 1.

21-FEB-200
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Matches 5
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   NUCLEOTIDE SEQUENCE Woods D.E., Nierman V Submitted (SEP-2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.; "Full-length cDNAs from chicken bursal lymphocytes to facil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-NOV-2004, sequence version 07-FEB-2006, entry version 6.
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Q5ZJM2;
                                                                                                                      Burkholderiaceae;
NCBI_TaxID=320372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Pfam; PF04420; CHD5; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORFNames=RCJMB04
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5; Conserv
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      ő
                                     [LARGE SCALE GENOMIC DNA]
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      the
      EMBL/GenBank/DDBJ databases
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Pred. No.
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Attribution-NoDerivs License
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                                                                                                                                                        MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Aklausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Allschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Allschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX A. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX A. Brownstein M.J., McKernan K.J., Malek J.A., Gunaratte P.H.,

XX A. Hopkins S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX A. Kichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX A. Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX A. Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX A. Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX A. Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X.,

XX A. Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X.,

XX A. Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X.,

XX A. Hilalon D.K., Touchman J.W., Green E.D., Dickson M.C.,

XX A. Hilalon D.K., Touchman J.W., Green E.D., Dickson M.C.,

XX A. Hilalon D.K., Touchman J.W., Green E.D., Dickson M.C.,

XX A. Hollon D.K., Krzywinski M.I., Skalska U., Smailus D.E.,

XX B. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

XX Generation and initial analysis of more than 15,000 full-length human

XX D. Hollon D. H. L., Touchman J.W., Green B.D., Dickson M.C.,

XX D. Hollon D.K., Muzny D.M., Marra M.A.;

XX D. Hollon D.K., Marra M.A.;

XX D. Hollon D.K., Muzny D.M., Muzny D.M., Muzny M.A.;

XX D. Hollon D.K., Muzny D.M., Muzny M.A.;

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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; CP000124; ABA48582.1; -; TIGR; BURPS1710b 2850; -. InterPro; IPR011633; DUF1602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q52KS6_XENLA
Q52KS6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
  Copyrighted
                                        Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
                                                               Klein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Eye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae;
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                                                                                  TISSUE=Eye;
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                                                               Gerhard D.S.;
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    UniProt
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  Consortium,
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Pred. No.
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C069DFC776D45162
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see http://www.uniprot.org/terms
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RESULT 46
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AC Q5AAF5 CANAC
Q5AAF5 CANAC
DT 26-APR-2
DT 26-APR-2
DT 07-FEB-2
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DT WFDOLhat
GN ORFNames
OS Candida
OC Candida
OC Saccharo
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Best Local
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InterPro; 1...
Fam; PF04420; Cr
                                                                                         26-APR-2005, integrated into UniProtKB/TrEMBL 26-APR-2005, sequence version 1. 07-FEB-2006, entry version 5. Hypothetical protein. GRFNames=Ca019.7533; Candida albicans SC5314. Eukaryota; Fungi; Ascomycota; Saccharomycoting Saccharomycotales; mitosporic Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
PubMed=15256591; DOI=10.1073/pnas.0403929101;
PubMed=15256591; Doi=10.1073/pnas.0403929101;
Nissen R.M., Sun Z., Swindell E.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-2004, integrated into UniProtKB/TrEMBL 16-AUG-2004, sequence version 1. 07-FBB-2006, entry version 9. pinball wizard.
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STRAIN=SC5314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/to
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6DRM0;
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                                                                       NCBI_TaxID=237561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ensembl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 101:12792-12797(2004)
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ZDB-GENE-030131-7696; wrb.
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                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                             [LARGE
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                             SCALE GENOMIC DNA]
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DB 2;
Pred. No. 2.2e+02
                                                                                                Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4F4350EB2C29184E CRC64;
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RX MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zsimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
RA Rammer J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
THE DNA sequence of human chromosome 21.";
UN Nature 405:311-319(2000).
UN [3]
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TISSUE-Ovary,
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.
Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Egeo A., Mazzocco M., Sotgia F., Arrigo P., Oliva R., Bergono Nizetic D., Rasore-Quartino A., Scartezzini P.; "Identification and characterization of a new human cDNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=15123810; DOI=10.1073/pnas.0401648101; Jones T., Federspiel N.A., Chibana H., Dungan Magee B.B., Newport G., Thorstenson Y.R., Agal Davis R.W., Scherer S.;
                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome 21q22.3 encoding a basic nuclear protein."; Hum. Genet. 102:289-293(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AACQ01000039; EAK99775.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The diploid genome sequence of Candida albicans.";
Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
-I- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                         NUCLEOTIDE
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RESULT
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Hobards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
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SEQUENCE
STRAIN=C57BL/6J; TISSUE=Corpus striatum;
PubMed=16141072; DOI=10.1126/science.1112014;
Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda I Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Bajic V.B., Wilming L.G., Aidinis V., Allen J., Cavolan M., Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WRB_MOUSE STANDARD; PRT; 174 AA.

QBKQDV; Q9D1W0;

Q0-MAY-2005, integrated into UniProtKB/Swiss-Prot.

Q1-QCT-2002, sequence version 1.

Q7-FEB-2006, entry version 18.

Tryptophan-rich protein.
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EMBL; AF064861; -; NOT ANNOTATED_CDS; Genomic_
EMBL; AL163279; CAB90454.1; -; Genomic_DNA.
EMBL; BC012415; AAH12415.1; -; mRNA.
Ensembl; ENGG00000182093; Homo sapiens.
H-InvDB; HIX0016117; -.
                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muroidea;
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GO; GO:0005634; C:nucleus;
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SUBCELLULAR LOCATION: Nucleus.
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19780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Glires; Rodentia; Sciurogna
                                                                                                                                                                                                                                                                                                                                                                                        [LARGE SCALE MRNA]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.30
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tryptophan-rich protein /FTId=PRO_000065979. F -> I (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A01F11CC564EAB6E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sciurognathi;
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RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G., RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., RA Fletcher C.F., Fukushima T., Furuno M., Fucaki S., Gariboldi M., Ra di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G., RA fletcher C.F., Fukushima T., Furuno M., Fucaki S., Gariboldi M., Ra Goorgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E., RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., RA Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T., RA Hill D., Huminiecki L., Iacono M., Kelso J., Kitamura H., RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J., Na Mateuda H., Matsuzawa S., Mishikawa S., Nori F., Ohara O., Nakauchi H., Ng P., Nishikawa S., Nori F., Ohara O., Ohara O., Nakauchi H., Ng P., Nishikawa S., Nori F., Ohara O., Pang K.C., Pavan W.J., Pavesi G., Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rot B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Ra Petrovsky N., Piazza S., Randelin A., Schneider C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Ra Shibata Y., Sinkada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Verardo R., Wei C.L., Yagi K., Tanki K., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Udda H.R., Zabaroysky E., Zhu S., Zimmer A., Hide W., Bult C., Ra Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Ra Kawashima T., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Ra Grimmond S., Matana T., Katona M., Suzuki M., Aoki J., Arakawa T., Ra Rayashizaki Y., Tanki K., Natomiya N., Ra Kawashima T., Kanama P., Saki D., Canamar A., Natomiya N., Ra Kayashira M., Natomiya N., Natomiya N., Natomiya N., Natomiya N., Natomiya N., Natomiy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Vallalon D.K., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science [2]
                          GO;
                                                  EMBL; AK021091; BAB32297.1; -; mRNA. EMBL; BC031769; AAH31769.1; -; mRNA. Ensembl; ENSMUSG000000023147; Mus mus. MGI; MGI:2136882; Wrb.
                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
STRAIN=FVB/N; TISSUE-Kidney;
MEDLINE=22388257; PubMed112477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                         Copyrighted
GO:0016021; C:integral erPro; IPR007514; CHD5.
                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Nucleus ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.
                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcriptional landscape of the mammalian nce 309:1559-1563(2005).
                                                                                                                                                                                                                                                                                 IsoId=Q8K0D7-2; Sequence=VSP_013643, VSP_013644; \
                                                                                                                                                                                                                                                                                                                                       IsoId=Q8K0D7-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                             splicing; Named
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A. 99:16899-16903(2002).
                          to membrane; TAS
                                                                                   musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
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WRB_RAT
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Best Local S
Matches 5
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Best Local :
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10-MAY-2005, integrated into UniProtKB/Swiss-Prot.
21-DEC-2004, sequence version 1.
07-FEB-2006, entry version 4.
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Alternative splicing; Nuclear CHAIN 1 174
                                                                                                          Q6P6S5;
10-MAY-2005, integrated into U
05-JUL-2004, sequence version
07-FEB-2006, entry version 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                             Rattus norvegicus (Rat).
                                                                    Name=Wrb;
                                                                                   Tryptophan-rich
                                                                                                                                                                                                WRB_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007514; CH
Pfam; PF04420; CHD5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; CR860481; CAH92603.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/teDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The German cDNA consortium; Submitted (NOV-2004) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tryptophan-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Nucleus (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lear protein.
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                                                                                                                                                                                                                                                                                                                                                                                            Similarity 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                       integrated into UniProtKB/Swiss-Prot
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                                                                                   protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19766 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [LARGE
Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Glires; Rodentia; Sciurogna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19867 MW
                                                                                                                                                                                                                                                                                                                                                                                                                   90.3%;
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Missing (In isoform 7
/mrd=VSP 013644.
/mrd=VSP 013644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tryptophan-rich protein.
/FTId=PRO_000065981.
; 0F1F0F3DB1D38202 CRC64;
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/FTId=PRO_0000065980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   see http://www.uniprot.org/terms
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                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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Ensembl; ENSRNOG00000001629; Rattus norvegicus.
RGD; 735104; Wrb.
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2 US-08-313-553-11
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Patent No. 6309877
GENERAL INFORMATION:
APPLICANT: Chau, Raymond M. W.
TITLE OF INVENTION: Isolation and Use of Mot FILE REFERENCE: 12592-2
CURRENT APPLICATION NUMBER: US/08/928,862
CURRENT FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 33
TYPE: PRT
ORGANISM: Homo sapiens
US-08-928-862-4
 US-09-592-018-4
; Sequence 4, Application US/09592018
; Patent No. 6759389
; GENERAL INFORMATION:
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US-08-928-862-4
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US-08-587-389-2
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US-08-011A-18
US-08-110-011A-18
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US-09-1312-870-3
US-09-131-934-1
US-09-522-737-66
US-09-522-737-66
US-09-529-994-1
US-09-509-994-2
US-09-653-274-10
US-09-653-274-10
US-09-653-274-10
US-09-332-769-44
US-09-712-363-180
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Pred. No.
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RESULT 4
US-09-198-452A-977
US-09-198-452A-977, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT; ORGANISM: Homo Sapiens US-09-989-481-4
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US-09-989-481-4
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Best Local (
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APPLICANT: Griffais, R. TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, frag
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis,
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
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TITLE OF INVENTION: Isolation and Use of Motoneurontropic Factors
FILE REFERENCE: 12592-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 08/9928862
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 08/751225
PRIOR EILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: US 60/026792
PRIOR FILING DATE: 1996-09-27
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CURRENT FILING DATE: 2001-11-20
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PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: US 60/026792
PRIOR FILING DATE: 1996-09-27
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TITLE OF INVENTION: Isolation and Use of Motoneurontropic Factors
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TYPE: PRT
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US-09-438-185A-906
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Matches
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PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 906
LENGTH: 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue
                                                                                                                                                                                                                          Sequence 60, Application US/08914375C Patent No. 6377893 GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
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CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR FILING DATE: 1998-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 357
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
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ORGANISM: Chlamydia pneumoniae
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
              ZIP: 32605-4147
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
                                                                                                                                                                        Applications of Protein Structure Predictions NUMBER OF SEQUENCES: 74
                                                                                                                                                                                                             APPLICANT: Steven A. Benner
                                                                                                                                                           CORRESPONDENCE ADDRESS
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6; Conserva
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                                                                                       STATE: FL
                                                                                                                     ADDRESSEE: Steven A. Benner STREET: 1501 NW 68th Terrace
COMPUTER: Apple MacIntosh
                                                                   COUNTRY: United States
                                                                                                        CITY: Gainesville
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100.0%; Pred. No. 6
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US-09-252-991A-23341
; Sequence 23341, Application US/09252991A
; Patent No. 6551795
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                                                                                                                                                                                                 RESULT 8
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23341
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Sequence 11070, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23341
LENGTH: 509
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Best Local Similarity
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILLING DATE: 1999-02-18
CURRENT FILLING DATE: 1999-02-18
CURRENT FILLING DATE: 1999-02-18
CURRENT FILLING DATE: 1999-02-18
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,375C
FILING DATE: 19-Aug-1997
CLASSIFICATION: 702/20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352 392 7773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: ascb_ecoli SEQUENCE DESCRIPTION: SEQ ID NO: 60:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: amino acid
ORIGINAL SOURCE:
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ilarity 100.0%;
Conservative (
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US-09-252-991A-32051
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US-09-252-991A-18159
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GENERAL INFORMATION:
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SEQ ID NO 11070
LENGTH: 188
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Best Local :
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LENGTH: 1778
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Best Local
SEQ ID NO 32051
LENGTH: 198
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                                                                                                                                                                     TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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PRIOR TILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                               CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
                                                     PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                          PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
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                                   NUMBER OF SEQ ID NOS:
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                                                                              Rubenfield et al.

NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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Pred. No. 1.4e+03;
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Pred. No. 1.4e+02;
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US-09-252-991A-32051
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PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 14027
LENGTH: ...
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14027, Application US/09489039A
                                                                                                                                                                                                                                                   APPLICANT: Gary Breton et. al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709-2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                   LENGTH: 387
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Pseudomonas aeruginosa
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FSRYAQ 116
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83.3%;
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                                                           Score 27; DB
Pred. No. 4.8e
1; Mismatches
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Pred. No. 4.5e+02;
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                                                                                         Length 387;
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RESULT 13

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; OTHER INFORMATION: axbb erwch; SEQUENCE DESCRIPTION: SEQ ID NO: 61: US-08-914-375C-61
                                                                                                                                                                                                                                                                                                                                         US-09-198-452A-638
; Sequence 638, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
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                                                                                                                     ; ORGANISM: Chlamydia
US-09-198-452A-638
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GENERAL INFORMATION:
                                                                                                                                                                    SEQ ID NO 638
LENGTH: 460
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                                                    Matches
                                                                  Query Match
Best Local
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                                                                                                                                                                                                   APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence
TITLE OF INVENTION: thereof and uses thereof, in particul
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                        TYPE: PRT
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OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,375C
FILING DATE: 19-Aug-1997
CLASSIFICATION INFORMATION:
TELEPHONE: 352 392 7773
TELEPHONE: 352 392 7773
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
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TOPOLOGY: linear
MOLECULE TYPE: amino acid
ORIGINAL SOURCE:
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ADDRESSEE: Steven
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                                                  Similarity
5; Conserv
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FSRYAR 6
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Pred. No. 5.
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in particular for the diagnosis,
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; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8224
; LENGTH: 469
; TYPE: PRT
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CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13505
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                                                                                         GENERAL INFORMATION:
APPLICANT: Dunn-Coleman, Nigel
APPLICANT: Goedegebuur, Frits
                                                                                                                                                       Sequence 2, Application US/10026140 Patent No. 7005289
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APPLICANT: Gary Br
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APPLICANT: Ward, Michael
APPLICANT: Yao, Jian
APPLICANT: Yao, Jian
TITLE OF INVENTION: BGL5 Beta-Glucosidase and Nucleic Acids
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: GC697
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
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Pred. No. 5.7e+02;
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Pred. No.
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; ORGANISM: Trichoderma reesei; FEATURE: ; NAME/KEY: VARIANT; LOCATION: (1)...(484); OTHER INFORMATION: Xaa = Any Amino US-10-026-140-2
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US-09-134-001C-4633
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LENGTH: 484
TYPE: PRT
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SEQ ID NO 4633
LENGTH: 538
TYPE: PRT
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APPLICANT: The Regents of the University of California TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence FILE REFERENCE: 018941-000411US CURRENT APPLICATION NUMBER: US/09/438,185A CURRENT FILING DATE: 2002-03-13 PRIOR APPLICATION NUMBER: US 60/108,279 PRIOR FILING DATE: 1998-11-12 PRIOR PILICATION NUMBER: US 60/128,606 PRIOR FILING DATE: 1999-04-08 NUMBER OF SEQ ID NOS: 1074
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CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                    APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue
APPLICANT: Davis, Ronald
APPLICANT: The Regents of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
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83.3%;
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Pred. No.
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Pred. No.
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RESULT 20
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US-09-438-185A-599
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SEQ ID NO 599
LENGTH: 579
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
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PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931478.0
PRIOR FILING DATE: 1999-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
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                                                                                                                                                       FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932227.9
FILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: DE 19932190.6 FILING DATE: 1999-07-09
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APPLICATION NUMBER: DE 19932125.6
FILING DATE: 1999-07-09
APPLICATION NUMBER: DE 19932128.0
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APPLICATION NUMBER: DE 19932124.8
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                                                    APPLICATION NUMBER: DE 19932230.9 FILING DATE: 1999-07-09
                                                                                        APPLICATION NUMBER: DE 19932229.5 FILING DATE: 1999-07-09
                                                                                                                         APPLICATION NUMBER: DE 19932228.7 FILING DATE: 1999-07-09
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                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: DE 19932182.5
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                APPLICATION NUMBER: DE 19932927.3 FILING DATE: 1999-07-14
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Zelder, Oskar
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NUMBER: DE 19933005.0
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83.3%;
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Pred. No. 7.2e+02;
0; Mismatches 1
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; ORGANISM: Human
US-09-949-016-10468
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US-09-949-016-10468
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LENGTH: 630
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GENERAL INFORMATION:
                                                                      SEQ ID NO 10468
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Best Local
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 600/237,768
                                                                                                 PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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                                    TYPE: PRT
                                                  LENGTH:
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FILING DATE: 1999-08-27
APPLICATION NUMBER: DE 19940830.0
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APPLICATION NUMBER: DE 19940833.5
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Pred. No. 7.9e+02;
0; Mismatches 1
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US-09-252-991A-29161
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                                                RESULT 24
US-09-543-681A-6207
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                ; Sequence 6207, Application US/09543681A
; Patent No. 6605709
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TITLE OF INVENTION: DICHOIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6106
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29161
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Matches 5; Conserva
GENERAL INFORMATION:
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Matches 5; Conserv
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                           ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                           LENGTH: 108
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83.3%;
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1; Mismatches 0;
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Pred. No.
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Pred. No. 8.5e+02;
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US-08-497-312-20
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US-08-497-312-20
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FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR TILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 6207

LENGTH: 111
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Best Local
                                    Query Match
   Matches
                     Best Local
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TELEX: 388961 1PM04UT
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: CU 80/94
FILING DATE: 30-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOND, LAURENCE B.
REGISTRATION NUMBER: 30,549
REFERENCE/DOCKET NUMBER: 2629U
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
STREET: 215 Y 15, ATABEY PLAYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/497,312
FILING DATE: 30-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 11600
                                                                                                                                 TOPOLOGY:
                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                 TELEPHONE: 801/532-1922
TELEFAX: 801/531-9168
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                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 FSRYER 54
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 Similarity 5; Conserv
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   Conservative
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                                                                                                                                   unknown
                                                                                             : protein
NO
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 83.9%; Score 26; DB 1; Lo
100.0%; Pred. No. 2.4e+02;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for obtaining modified immunoglobulins with reduced immunogenicity of murine
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Pred. No. 2.2e+02;
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                                        Length 119;
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US-08-497-312-22
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Matches
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APPLICANT:
APPLICANT:
                                                                                                                               Sequence 1, Application US/08875674A Patent No. 6572857
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                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,312
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 80/94
FILING DATE: 30-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOND, LAURENCE B.
REGISTRATION NUMBER: 30,549
REFERENCE/DOCKET NUMBER: 2629US
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TELEX: 388961 1PM04UT
INFORMATION FOR SEQ ID NO:
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APPLICANT:
             APPLICANT: SIERRA
APPLICANT: TORMO I
TITLE OF INVENTION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 801/532-1922
TELEFAX: 801/531-9168
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                 Local Similarity hes 5; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: un
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STREET: 215 Y 15, ATABEY PLAYA
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                                                                                                                 INFORMATION:
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          SIERRA BL ZQUEZ, P.
TORMO BRAVO, B. R.
VENTION: Anti-CD6 monoclonal antibodies
                                                           LOMBARDERO VALLADARES,
P REZ RODR GUEZ, R.
                                                                                                 MONTERO
                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30 (EPO)
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                                                                                               CASIMIRO, J. E.
                                                                                                                                                                                                                                                                                                                 83.9%; Score 26;
100.0%; Pred. No.
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               and their uses
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OTHER INFORMATION: Sequence corresponding to the variable region Patent No. 6572857
                                                                                                                                                                                                Sequence 3, Application US/08875674A Patent No. 6572857
                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (914) 723-4300
TELEFAX: (914) 723-4301
INFORMATION FOR SEQ ID NO: 1:
AFFLICANT: LOMBARDERO VALLADARES, J.
APPLICANT: P REZ RODR GUEZ, R.
APPLICANT: SIERA BL ZQUEZ, P.
APPLICANT: TORMO BRAVO, B. R.
TITLE OF INVENTION: Anti-CD6 monoclonal antibodies and their uses
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lackenbach Ci---
                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SENSE: NO
FRAGMENT TYPE: -N Terminal fragment.
ORIGINAL SOURCE:
ORGANISM: Mice period
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mice Balb/C
INDIVIDUAL ISOLATE: ior tlA
TISSUE TYPE: Murine hibridoma
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CU96/00004
FILING DATE: 18-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: HENRY A. MARZULLO, JR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE Floppy disk 3.5' (1.4 MB).
COMPUTER: Compatible PC IBM (80486, 8 M Ram).
OPERATING SYSTEM: Windows 95.
SOFTWARE: Word Perfect 5.0 for Windows 95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: VII.
STREET: VII.
STREET: VII.
STREET: New York
"I S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (914) 723-4300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Word Perfect 5.0 for Windows 95 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: Amino a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 20,910
REFERENCE/DOCKET NUMBER: P-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                  29 FSRYA 33
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Amino acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
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                                                                                                                                                                                                                                                                                                                                                                                                             83.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the heavy chain of the monoclonal antibody recognizing \mbox{hum.} designated as sub-clone for tlA.
                                                                                                                                                                                                                                                                                                                                                                                                             Score 26; DB 2; I
; Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD: By similarity with known sequence.
OTHER INFORMATION: Sequence corresponding to the humanized
Patent No. 6572857
OTHER INFORMATION: variant of sub-clone for tla recognizing
OTHER INFORMATION: to the variable region of its heavy chain
                                                                                                                                                                                                                                                   Sequence 51, Application US/10118100 Patent No. 6989250
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                  TITLE OF INVENTION: A Method For In Vitro TITLE OF INVENTION: Evolution of Protein FILE REFERENCE: Mewburn 341711 CURRENT APPLICATION NUMBER: US/10/118,100 CURRENT FILING DATE: 2002-04-08 PRIOR APPLICATION NUMBER: US/09/341,711 PRIOR FILING DATE: 1999-09-21
                                                                                                                                                                      APPLICANT: BioInvent International AB APPLICANT: Soderlind, Ulf APPLICANT: Borrebaeck, Carl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 18-NOV-1996
ATTORNEY AGENT INFORMATION:
NAME: HENRY A. MARZULLO, JR.
REGISTRATION NUMBER: 20,910
REFERENCE/DOCKET NUMBER: P-12
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (914)-723-4301
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE:
ORIGINAL SOURCE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: PCT/CU96/00004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word Perfect 5.0 for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,674A
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MEDIUM TYPE: Floppy disk 3.5' (1.4 MB).
COMPUTER: Compatible PC IBM (80486, 8 M Ram).
OPERATING SYSTEM: Windows 95.
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Terminal fragment.
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APPLICATION NUMBER: PCT/GB98/00219 FILING DATE: 1998-01-26
                                                                                                                                                                                                                                                                                                                                                                       29 FSRYA 33
                                                                                                                                                                                                                                                                                                                                                                                                            1 FSRYA 5
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SO " SP 2/0 " CHO
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                                                                                                                                  Molecular
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US-09-270-767-36842
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                                                                   US-09-270-767-36842
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PRIOR FILING DATE: 1997-01-24
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 51
LENGTH: 130
TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 44176

LENGTH: 131
                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILLING DATE: 1999-03-17
CURRENT FILLING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36842
LENGTH: 165
                                                                                                                                                                                                                                                                                                                      Sequence 36842, Application US/09270767 Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local
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Best Local Similarity
Matches 5; Conserv
                                 Query Match
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                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                 OTHER INFORMATION: Xaa means any amino acid
                                                                                                    FEATURE:
                                                                                                                 ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 FSRYA 41
                                                                                                                                                                                                                                                                                                                                                                                                                           96 FSRYA 100
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83.9%; Score 26; DB 2; llarity 100.0%; Pred. No. 3.3e+Conservative 0; Mismatches
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Pred. No. 2.6e+02;
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 3.3e+02;
hes 0;
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RESULT 34
US-09-549-108-11
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Best Local Similarity
"~+~hes 5; Conserve
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; ORGANISM: BR449
US-09-248-528-11
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US-09-270-767-52059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 52059
               Sequence 11, Application US/09549108 Patent No. 6214603 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/09248528C Patent No. 6153415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 52059, Application US/09270767 Patent No. 6703491
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Best Local (
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APPLICANT: Padmakumar, Rugmini
APPLICANT: Padmakumar, Rugmini
APPLICANT: Eddmakumar, Rugmini
APPLICANT: Kim, Sang H
TITLE OF INVENTION: Method for Producing Amide Compounds Using a
TITLE OF INVENTION: Hydratase from a Thermophilic Bacillus
FILE REPERENCE: MSU 4.1.401
CURRENT APPLICATION NUMBER: US/09/248,528C
CURRENT APPLICATION NUMBER: US/09/248,528C
CURRENT FILING DATE: 1999-02-10
EARLIER FILING DATE: 1999-04-29
RUMBER OF SEQ ID NOS: 18
COMMANDER: DESCRIPTION OF SEQ ID NOS: 18
APPLICANT:
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TYPE: PRT
ORGANISM: Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                         ENGTH: 229
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Oriel, Patrick J
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                                                                                                                                                                                                                            83.9%;
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Pred. No. 4.6e
0; Mismatches
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3.3e+02;
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FILE REFERENCE: MSU 4.1-486
CURRENT APPLICATION NUMBER: US/09/549,108
CURRENT FILING DATE: 200-04-13
PRIOR APPLICATION NUMBER: 60/083,485
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 09/248,528
PRIOR APPLICATION NUMBER: 09/248,528
PRIOR FILING DATE: 1999-02-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Oriel, Patrick J
APPLICANT: Padmakumar, Rugmini
APPLICANT: Kim, Sang H
ITITLE OF INVENTION: Method for Producing Amide Compounds Using a l
ITITLE OF INVENTION: Method for Producing Amide Compounds Using a l
ITITLE OF INVENTION: Hydratase from a Thermophilic Bacillus
FILE REFERENCE: MSU 4.1-489
CURRENT APPLICATION NUMBER: US/09/549,111
CURRENT FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/083,485
PRIOR APPLICATION NUMBER: 09/248,528
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1999-02-10
NUMBER OF SEQ ID NOS: 18
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; ORGANISM: BR449
US-09-549-108-11
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US-09-549-111-11
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SOFTWARE: Pact
SEQ ID NO 11
FORGTH: 229
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Best Local S
Matches 5
                                                                                                                 Sequence 11, Application US/09549106
Patent No. 6242242
GENERAL INFORMATION:
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Best Local (
                APPLICANT: Oriel, Patrick J
APPLICANT: Padmakumar, Rugmini
APPLICANT: Kim, Sang H
TITLE OF INVENTION: Method for
TITLE OF INVENTION: Hydratase
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APPLICANT: Kim, Sang H
TITLE OF INVENTION: Method for Producing Amide Compounds U:
TITLE OF INVENTION: Hydratase from a Thermophilic Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 22
TYPE: PRT
    FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: BR449
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5; Conserv
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ION: Method for Producing Amide Compounds Using ION: Hydratase from a Thermophilic Bacillus MSU 4.1-487
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Pred. No. 4.6e
0; Mismatches
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Pred. No. 4.6e+02;
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. 4.6e+02;
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; LENGTH: 229
; TYPE: PRT
; ORGANISM: BR449
US-09-549-106-11
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; ORGANISM: BR449
US-09-550-394-11
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SEQ ID NO 11
LENGTH: 229
NUMBER OF SEQ ID NOS:
SEQ ID NO 12718
LENGTH: 233
                                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local
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SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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APPLICANT:
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Patent No. 6287828
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PRIOR APPLICATION NUMBER: 09/2
PRIOR FILING DATE: 1999-02-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
PEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                   FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                           APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/550,394
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/083,485
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 09/248,528
PRIOR FILING DATE: 1999-02-10
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Padmakumar, Rugmini
APPLICANT: Kim, Sang H
TITLE OP INVENTION: Method for Producing Amide Compounds Using a
TITLE OF INVENTION: Hydratase from a Thermophilic Bacillus
FILE REFERENCE: MSU 4.1-488
CHEBERENCE: MSU 4.1-488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/549,106
CURRENT FILING DATE: 2000-04-13
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les 5; Conservative
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                                                                                                                                                                                                                                                                                                                                             161 FPRYAR 166
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83.3%;
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Pred. No. 4.60
0; Mismatches
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Pred. No. 4.6e+02
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                        ; ORGANISM: Human
US-09-949-016-9375
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US-09-949-016-9375
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; ORGANISM: Human
US-09-949-016-6472
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US-09-949-016-6472
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6472
LENGTH: 252
                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CLOO1307
CURRENT APPLICATION UNBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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Patent No. 6812339
                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9375
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9375, Application US/09949016 Patent No. 6812339
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Matches 5; Conserv
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  Query Match
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CRICK APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-09-08
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                                                                                 TYPE: PRT
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83.3%;
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; Pred. No. 4.7e+02;
0; Mismatches 0;
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  Score 26;
  DB
  2
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OF DETECTION AND USES THEREOF
Length 253;
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APPLICANT: Kalman, Sue
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
ITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT FILING DATE: 018941-000411US
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-438-185A-256
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Best Local Similarity
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US-09-198-452A-266
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GENERAL INFORMATION:
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Matches 5; Conservative
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LENGTH: 270
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                                                                                                                               TYPE: PRT
ORCANISM: Chlamydia pneumoniae
FEATURE:
OTHER INFORMATION: CPn0254
-09-438-185A-256
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TITLE OF INVENTION: Chereof and uses thereof, in particular for the diagnos TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnos TITLE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999 CURRENT EPPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Stephens, Richard APPLICANT: Mitchell, Wayne APPLICANT: Kalman, Sue
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TYPE: PRT
ORGANISM: Chlamydia pneumoniae
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150 FSRYA 154
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                                 FSRYA 5
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100.0%; Pred. No.
tive 0; Mismatc
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                                                                     Mismatches
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                                                                                    DB 2; Le 5.5e+02;
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Best Local Similarity
'---hes 5; Conserv:
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US-08-944-483-66
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US-09-252-991A-20485
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US-09-252-991A-25159
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.136
                                                                                            Sequence 66, Application US/08944483 Patent No. 6232456 GENERAL INFORMATION:
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Matches
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LENGTH: 283
TYPE: PRT
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LENGTH: 276
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                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
                                                         APPLICANT:
APPLICANT:
                   APPLICANT:
                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                              64 WSRYAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 FHRYAR 76
                                                                                                                                                                                                                                                               1 FSRYAR 6
                                                                                                                                                                                                                                                                                                   . Similarity 5; Conserv
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COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GRANADOS, EDWARD N.
KLASS, MICHAEL R.
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1998-02-18
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                                                                                                                                                                                                                                                                                                   Score 26; DB 2;
Pred. No. 5.7e+02;
1; Mismatches 0
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Pred. No. 5.6e+02;
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; ORGANISM: Candida albicans US-09-248-796A-14594
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                                                                                        APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14594
LENGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14594, Application US/09248796A Patent No. 6747137 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ITTLE OF INVENTION: ITTLE OF INVENTION: INVENT
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 61
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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STRANDEDNESS: sir
TOPOLOGY: linear
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REGISTRATION NUMBER: 35,441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSRYAR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 amino acids
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100 Abbott Park Road
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STEVEN D.
STEVEN D.
NOVEL SERINE PROTEASE REAGENTS
AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.9%;
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Pred. No. 6.1e
0; Mismatches
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APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 319
TYPE: DPT
                                                                                                                                           CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 14005

LENGTH: 327

TYPE: PRT

ORGANISM: Klebsiella pneumoniae
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US-09-386-642-12
; Sequence 12, Application US/09386642
"""" No. 6420157
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US-09-489-039A-14005
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Best Local
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Best Local
                                                            Best Local Similarity
Matches 5; Conserv
                                                                                               Query Match
                                                                                                                                                                                                                                                                                                            APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                   FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Fusion OTHER INFORMATION: with homo sapien serine protease catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 FSRYIR 149
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251 WSRYAR
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                               1 FSRYAR 6
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                                                                  Conservative
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100.0%;
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83.3%;
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Pred. No.
                                                                Score 26; DB 2; Le
Pred. No. 6.6e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26; DB 2;
Pred. No. 6.5e+02;
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. 6.2e+02;
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                                                                                                 Length 327;
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RESULT 49 US-09-386-642-11 Garuence 11, Application US/09386642

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APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: O, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION UNMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SQ ID NO 11
LENGTH: 328
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
OTHER INFORMATION: with homo sapien serine protease catalytic domain
US-09-386-642-11
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue
APPLICANT: Kalman, Sue
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 0.18941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
FRIOR APPLICATION NUMBER: US 60/108,279
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 960
SEQ ID NO 960
SEQ ID NO 960
CHENTER: CREASES
CRUES INFORMATION. CREASES
Search completed: August 29, 2006, 06:17:52 Job time : 14.3366 secs
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US-09-438-185A-960
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                                                                                                                                                                                          Query Match 83.9%; Score 26; DB 2; Length 337; Best Local Similarity 83.3%; Pred. No. 6.8e+02; Matches 5; Conservative 0; Mismatches 1; Indels
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RESULT 4
US-10-541-343-6
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; Publication No. US20060052299A1
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Publication No. US20060052299A1
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                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic peptide -10-541-343-5
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PRIOR FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: 60/441,722
PRIOR FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 7
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APPLICANT: Ko, Pui-Yuk Dorothy
TITLE OF INVENTION: MNTF Peptides and Compositions and Methods
FILE REFERENCE: 2001-103US
CURRENT APPLICATION NUMBER: US/10/541,343
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: PCT/US2004/001468
PRIOR APPLICATION NUMBER: PCT/US2004/001468
PRIOR FILING DATE: 2004-01-21
PRIOR PPLICATION NUMBER: 60/441,722
PRIOR FILING DATE: 2003-01-21
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APPLICANT: Ko, Pui-Yuk Dorothy
TITLE OF INVENTION: MOTE Peptides and Compositions and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 2001-103US
CURRENT APPLICATION NUMBER: US/10/541,343
CURRENT FILING DATE: 2005-07-05
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                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial
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OTHER INFORMATION: Synthetic peptide
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CURRENT APPLICATION NUMBER: US/10/541,343
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: PCT/US2004/001468
PRIOR FILING DATE: 2004-01-21
PRIOR FILING DATE: 2003-01-21
PRIOR FILING DATE: 2003-01-21
VUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 6
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                                Sequence 4, Application US/09989481
Publication No. US20020086831A1
GENERAL INFORMATION:
APPLICANT: Chau, Raymond M.W.
TITLE OF INVENTION: Isolation and Use of Motoneurontropic Factors
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APPLICANT: Chau, Raymond Ming Wah
APPLICANT: KO, Pui-Yuk Dorothy
TITLE OF INVENTION: MNTF Peptides and Compositions and Methods of Use
FILE REFERENCE: 2001-103US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.3 SEQ ID NO 7
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APPLICANT: Ko, Pui-Yuk Dorothy
TITLE OF INVENTION: MNTF Peptides and Compositions and Methods of Use
FILE REFERENCE: 2001-103US
CURRENT APPLICATION NUMBER: US/10/541,343
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: PCT/US2004/001468
PRIOR APPLICATION NUMBER: PCT/US2004/001468
PRIOR PILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: 60/441,722
PRIOR APPLICATION NUMBER: 60/441,722
PRIOR FILING DATE: 2003-01-21
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FILE REFERENCE: 12592-4
CURRENT APPLICATION NUMBER: US/09/989,481
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TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic peptide
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Pred. No.
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US-10-858-286-4
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US-10-858-545-4
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-989-481-4
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                                                                                                            Sequence 4, Application US/10858286
Publication No. US20040242486A1
GENERAL INFORMATION:
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Publication No. US20040224894A1
GENERAL INFORMATION:
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Matches 6; Conserv
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PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 08/751225
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: US 60/026792
PRIOR FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 5
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APPLICANT: Chau, Raymond M.W.
TITLE OF INVENTION: Isolation and Use of Motoneurontropic Factors
FILE REFERENCE: 12592-3
CURRENT APPLICATION NUMBER: US/10/858,286
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US/09/592,018
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PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 08/9928862
PRIOR EILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 08/751225
PRIOR FILING DATE: 1996-11-15
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CURRENT APPLICATION NUMBER: US/10/858,545
CURRENT FILING DATE: 2004-06-01
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ORGANISM: Homo Sapiens
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LENGTH: 33
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Publication No. US20060025565A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 6; Conserv
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                                        FILE REFERENCE: 12592-3
CURRENT APPLICATION NUMBER: US/10/858,144
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US/09/592,018
PRIOR FILING DATE: 2000-06-12
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PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 08/9928862
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 08/751225
PRIOR FILING DATE: 1996-11-15
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CURRENT APPLICATION NUMBER: US/10/858,543
CURRENT FILING DATE: 2004-06-01
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TITLE OF INVENTION: Isolation and Use of Motoneurontropic Factors
FILE REFERENCE: 12592-3
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PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 08/751225
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: US 60/026792
PRIOR FILING DATE: 1996-09-27
PRIOR FILING DATE: 1996-09-27
PRIOR FILING DATE: 1996-09-27
PRIOR FILING DATE: 1996-09-27
                                                                                                                               APPLICANT: Chau, Raymond M.W. TITLE OF INVENTION: Isolation and Use of Motoneurontropic Factors FILE REFERENCE: 12592-3
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NUMBER OF SEQ ID NOS: 5
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PRIOR APPLICATION NUMBER: US 08/9928862 PRIOR FILING DATE: 1997-09-12
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TYPE: PRT
ORGANISM: Homo Sapiens
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GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILLING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
SEQ ID NO 11746
LENGTH: 125
TYPE: PRT
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-858-144-4
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US-11-188-298-11746
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Best Local Similarity
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PRIOR FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: 60/441,722
PRIOR FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 7
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TYPE: PRT
ORGANISM: Artificial
FEATURE:
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APPLICANT: Ko, Pui-Yuk Dorothy
TITLE OF INVENTION: MNTF Peptides and Compositions and Methods of Use
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PRIOR APPLICATION NUMBER: US 60/026792
PRIOR FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 5
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CURRENT FILING DATE: 2005-07-05
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           ORGANISM: Desulfitobacterium hafniense
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Pred. No. 12;
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                                                        US-10-289-762-977
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US-10-289-762-977
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PRIOR FILING DATE: 2000-07-11
PRIOR PPLICATION NUMBER: 0017983.8
PRIOR APPLICATION NUMBER: 0017983.8
PRIOR TILING DATE: 2000-07-21
PRIOR PLING DATE: 2000-08-07
PRIOR PPLICATION NUMBER: 0020440.4
PRIOR PPLICATION NUMBER: 0020440.4
PRIOR PPLICATION NUMBER: 0020583.9
PRIOR APPLICATION NUMBER: 0027549.5
PRIOR APPLICATION NUMBER: 0027549.5
                                                                                                                                                                                                                     Sequence 977, Application US/10289762
Publication No. US20040006218A1
GENERRAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve-
TITLE OF INVENTION: and treatment of infection
                                                                                                                           FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 977
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SEQ ID NO 107
LENGTH: 357
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Best Local Similarity
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Query Match
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TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
FILE REFERENCE: PO25035WO
CURRENT APPLICATION NUMBER: US/10/312,273
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 0016363.4
PRIOR FILING DATE: 2000-07-03
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NUMBER OF SEQ ID NOS: 664
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                                                                        TYPE: PRT ORGANISM: Chlamydia pneumoniae
                                                                                                             LENGTH: 357
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Pred. No. 1.3e+02;
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Pred. No.
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Pred. No. 1.3e+02;
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Mismatches
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RESULT 16
US-10-437-963-176098
; Sequence 176098, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
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Best Local Similarity
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOPTWARE: PatentIn version 3.1
SEQ ID NO 54956
LENGTH: 357
TYPE: PRT
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APPLICANT: Zamuc
APPLICANT: Malor
APPLICANT: La Rosa, Thomas APPLICANT: Kovalic, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-10-23
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Malone, Cheryl
Haselbeck, Robert
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Zyskind, Judith
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Carr, Grant
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Pred. No. 1.3e+02;
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10 (52052) B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 23258 LENGTH: 463
Sequence 1759, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION UMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
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US-10-369-493-23258
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 176098
LENGTH: 412
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Publication No. US20030233675A1
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Best Local (
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6; Conserva
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Wu, Wei
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Pred. No. 1.5e+02;
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; ORGANISM: Bacillus subtilis subsp. subtilis str. 168
US-11-188-298-12707
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US-11-188-298-12707
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-05-23
PRIOR PILLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (53452) B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
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LENGTH: 463
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Publication No. US20060075522A1
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                                                                                                                                                                                                                           APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
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TYPE: PRT
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Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                       Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                             Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 31; DB 6; Length 463; ilarity 100.0%; Pred. No. 1.6e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09815242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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APPLICANT: Hyseq, Inc
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POI
FILE REFERENCE: 790C1P3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-31
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOPTWARE: CUStom
SEQ ID NO 54803
LENGTH: 1225
TYPE: PRT
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US-10-369-493-23518
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US-10-369-493-23518
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US-09-815-242-10270
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US-10-450-763-54803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 23518
LENGTH: 474
                                                                                                                                                                                                                                                                                                                Sequence 54803, Application US/10450763 Publication No. US20050196754A1 GENERAL INFERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23518, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10270
LENGTH: 474
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Best Local
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APPLICANT: Hinkle, Gree
APPLICANT: Slater, Ste
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PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100 6; Conservative
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Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
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Pred. No. 1.7e+02;
; Mismatches 0;
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FILTE OF INVESSION: NOTE: TITLE OF INVESSION: NUMBER: US/10/450,763;
CURRENT APPLICATION NUMBER: US/10/450,763;
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631;
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 55178
FENCHUM NO 55178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-450-763-55178; Sequence 55178, Application US/10450763; Publication No. US20050196754A1
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RESULT 24
US-10-424-599-186222
Sequence 186222, Application US/10424599
; Publication No. US20040031072A1
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Best Local Similarity
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo say
FEATURE:
NAME/KEY: DOMAIN
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NAME/KEY: DOMAIN
LOCATION: (332)..(380)
LOCATION: Tetrahydrofolate dehydrogenase/cyclohydrolase proteins domain
OTHER INFORMATION: identified by eMATRIX, accession number BL00766C, p-value=1.000e-
OTHER INFORMATION: 40, raw score of 25.86
                                                                                                                                                                                                                                                                                                            NAME/KEY: DOMAIN
LOCATION: (267)..(471)
LOCATION: Tetrahydrofolate dehydrogenase/cycloh domain identified by
OTHER INFORMATION: PFam, accession name THF_DHG_CYH, E-value=2.9e-134, PFam score
OTHER INFORMATION: 459.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (7)..(211)
OTHER INFORMATION: Tetral
OTHER INFORMATION: PFam,
OTHER INFORMATION: 460.9
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LOCATION: (7)..(
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                                                                                                                                                                                                                              Score 31; DB 5;
Pred. No. 4.4e+02;
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                  Length 1258;
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US-10-424-599-146582
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                                                                                                                                                          RESULT 26
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Sy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                          Sequence 265564, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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LENGTH: 67
TYPE: PRT
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Best Local Similarity
Matches 5; Conserv
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SEQ ID NO 146582
LENGTH: 79
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Matches 5; Conserv
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322))B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                        APPLICANT: La Rosa Thomas APPLICANT: Kovalic David
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APPLICANT: Kovalic David K
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LOCATION: (1)..(67)
OTHER INFORMATION: unsure at
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Glycine max
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Kovalic David K
Zhou Yihua
Cao Yongwei
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Pred. No. 1.4e+02;
1; Mismatches 0
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Pred. No. 1.1e+02;
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APPLICANT:

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APPLICANT: Tarczynski Mitchell C.
TITLE OF INVENTION: Alteration Of Oil Traits In
FILE REFERENCE: BB1458 US NA
CURRENT APPLICATION NUMBER: US/10/183,687
CURRENT FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: 60/301,913
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 532
SOFTWARE: Microsoft Office 97
SEQ ID NO 178
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US-10-424-599-265564
                                                                                     ; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (85)
; OTHER INFORMATION: Xaa =
US-10-183-687-178
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 265564
LENGTH: 85
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                                          Query Match
Best Local
                                                                                                                                                       FEATURE:
NAME/KEY: UNSURE
LOCATION: (80)
OTHER INFORMATION: Y
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APPLICANT:
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APPLICANT:
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APPLICANT: Allen, Will
APPLICANT: Cahoon, Reb
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ORGANISM: Glycine max
FEATURE:
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                                                                                                                                                                                                                    ORGANISM: Oryza sativa
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5; Conserv
 1 FSRYAR 6
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5; Conserv
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Shen, Bo
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Harvell, Leslie T.
Jones, Todd
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Oliveira, Igor Cunha
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1; Mismatches
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                                          Score 28; I
Pred. No. 1.
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                                          DB 4;
1.5e+02;
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APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21 (53222) B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 219020

LENGTH: 91

TYPR: ""
US-10-767-701-43382
Sequence 43382, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
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US-10-767-701-51064
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (55353) B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 51064
LENGTH: 123
TYPE: PRT
ORGANISM: Sorghum bicolor
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Best Local
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Pred. No. 2.1e+02;
1; Mismatches (
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APPLICANT: Kovalic, David K.

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                                                                                                                                                                                                                                                                                                            APPLICANT: Tarczyński, Mitchell C.
TITLE OF INVENTION: Alteration Of Oil Traits In Plants
FILE REFERENCE: BB1458 US NA
CURRENT APPLICATION NUMBER: US/10/183,687
CURRENT FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: 60/301,913
PRIOR APPLICATION NUMBER: 60/301,913
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 532
SOFTWARE: Microsoft Office 97
SEQ ID NO 174
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LENGTH: 124
TYPE: PRT
ORGANISM: Sorghum bicolor
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                                                                                                                                          FEATURE:
NAME/KEY: UNSURE
102)
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                                                                                                                                                                                                                                             LENGTH: 132
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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                                                                                                                              LOCATION: (102)
OTHER INFORMATION:
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OTHER INFORMATION:
             OCATION:
                                  NAME/KEY: UNSURE
                                                                                NAME/KEY: UNSURE LOCATION: (116)
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Local Similarity 83.3%;
les 5; Conservation
 INFORMATION:
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Oliveira, Igor Cunha
Sakai, Hajime
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Harvell, Leslie T.
Jones, Todd
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Klein, Ted
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Xaa
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any amino acid
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Pred. No. 2.1e+02;
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; NAME/KEY: UNSURE
; LOCATION: (122)
; OTHER INFORMATION: X
FEATURE:
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (125)
; OTHER INFORMATION: X
US-10-183-687-174
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Best Local Similarity
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US-10-501-282-480
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US-10-501-282-478
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LENGTH: 145
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/501,282 CURRENT FILING DATE: 2004-07-09 PRIOR APPLICATION NUMBER: 60/333,777 PRIOR FILING DATE: 2001-11-29 PRIOR APPLICATION NUMBER: 60/426,742 PRIOR FILING DATE: 2002-11-18
                                                                                                                      TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC FILE REFERENCE: AM100780 L2
                                                                                                                                                                                APPLICANT: MCMICHAEL, JOHN CALHOUN
APPLICANT: ZAGURSKY, ROBERT JOHN
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: FLETCHER, LEAH DIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/333,777
PRIOR TILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 60/426,742
PRIOR FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: PCT/US02/36123
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 6653
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CURRENT APPLICATION NUMBER: US/10/501,282
CURRENT FILING DATE: 2004-07-09
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APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: FLETCHER, LEAM DIANE
TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MCMICHAEL, JOHN CALHOUN
APPLICANT: ZAGURSKY, ROBERT JOHN
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: FLETCHER, LEAH DIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.2
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Pred. No. 2.5e
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2.5e+02;
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RESULT 34
US-09-984-245-156
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LENGTH: 172
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PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 6653
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TITLE OF INVENTION: 87 Human Secreted Proteins
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CURRENT FILING DATE: 2001-10-29
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PRIOR FILING DATE: 1998-03-19
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APPLICATION NUMBER: US 60/041,276
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APPLICATION NUMBER: US 60/048,069
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APPLICATION NUMBER: US 60/048,188
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APPLICATION NUMBER: US 60/048,096
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FILING DATE: 1997-05-3
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PRIOR APPLICATION NUMBER: US 09/154,707
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PRIOR APPLICATION NUMBER: US 60/060,862
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
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PRIOR APPLICATION NUMBER: PCT/US98/05311
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TYPE: PRT
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FILING DATE: 1997-05-30 APPLICATION NUMBER: US 6
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Pred. No. 2.9e+02
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; TYPE: PRT
; ORGANISM: Homo sapiens
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LENGTH: 174
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Publication No. US20
GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-03-19
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PRIOR APPLICATION NUMBER: US 60/042,344
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PRIOR FILING DATE: 1998-09-17
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CURRENT FILING DATE: 2001-10-29
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TITLE OF INVENTION: 87 Human Secreted Proteins
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FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,160
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,351
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FILING DATE: 1997-03-21
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APPLICATION NUMBER: US 60/042,344
FILING DATE: 1997-03-21
APPLICATION NUMBER: US 60/041,276
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FILING DATE: 1997-08-19
APPLICATION NUMBER: US 60/060,862
FILING DATE: 1997-10-02
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APPLICATION NUMBER: US 60/054,804
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APPLICATION NUMBER: US 60/048,099
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APPLICATION NUMBER: US 60/048,187
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Pred. No.
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2.9e+02;
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RESULT 37
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PRIOR APPLICATION NUMBER: US/09/966, 262
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: US 60/041, 277
PRIOR APPLICATION NUMBER: US 60/042, 344
PRIOR FILING DATE: 1997-03-21
PRIOR PRIOR APPLICATION NUMBER: US 60/042, 344
PRIOR FILING DATE: 1997-03-21
PRIOR PRIOR APPLICATION NUMBER: US 60/041, 276
PRIOR PRILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: US 60/041, 281
PRIOR PRILING DATE: 1997-03-21
PRIOR PRILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048, 094
PRIOR APPLICATION NUMBER: US 60/048, 350
PRIOR APPLICATION NUMBER: US 60/048, 350
PRIOR APPLICATION NUMBER: US 60/048, 350
PRIOR PRILING DATE: 1997-05-30
PRIOR PRILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048, 188
PRIOR PRILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048, 135
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PRIOR PRILING DATE: 1997-05-30
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PRIOR PRILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/048, 135
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Best Local S
Matches 5
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LENGTH: 174
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CURRENT FILING DATE: 2002-01-31
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NUMBER OF SEQ ID NOS: 343
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ORGANISM: Homo
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APPLICATION NUMBER: US
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APPLICATION NUMBER: US 60/048,096
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5. US20030018180A1
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83.3%;
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APPLICATION NUMBER: US 60/048,186 FILING DATE: 1997-05-30

APPLICATION NUMBER: US 60/048,352 FILING DATE: 1997-05-30

FILING DATE: 1997-05-

APPLICATION NUMBER: US 60/048,099

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US-10-143-090-156
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                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 156
                                                                                                                                                                                                                                                                                                                                                                       Sequence 156, Application US/10143090
Publication No. US20030069406A1
GENERAL INFORMATION:
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Best Local (
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                                                                                 Query Match
Best Local :
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                                                                  Matches
                                                                                                                                                                                                                                                                                  APPLICANT: Young et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REPERENCE: PZOO4P1
CURRENT APPLICATION NUMBER: US/10/143,090
CURRENT FILING DATE: 2002-05-13
                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/154,707
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 343
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: US 60/060,862
FILING DATE: 1997-10-02
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APPLICATION NUMBER: US 60/048,095
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Similarity 83.3%;
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FARYAR 74
                                                                  Conservative
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83.3%;
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Pred. No. 2.9e+02;
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Pred. No. 2.9e+02;
                                                                Mismatches
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RESULT 39
US-10-960-251-156
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US-10-437-963-197182
                                                                            APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 197182
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 10/143,090
PRIOR FILING DATE: 2002-05-13
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PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: PCT/US98/05311
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/041,277
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: 60/042,344
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CURRENT FILING DATE: 2004-10-08
                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: PZ004P1C3
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PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: 60/041,281
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                                          TYPE: PRI
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                    ORGANISM: Oryza sativa
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FEATURE:
                                                               LENGTH: 179
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                                                                                                                                                                                                                                                                                                   Cao, Yongwei
Wu, Wei
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5. US20050089911A1
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Pred. No. 2.9e+02;
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US-10-425-115-314441
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US-11-096-568A-9600
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                                                                                                                        US-10-425-115-314441
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APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 9600
                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 314441
LENGTH: 234
TYPE: PRT
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Matches
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LOCATION: (1)...(225)
OTHER INFORMATION: Ceres Seq. ID no. 12614812
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ORGANISM: Triticum aestivum
FEATURE:
                                                                                                                                    OTHER INFORMATION: Clone ID: MRT4577_4982C.1.peg
                                                                                                                                                    ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 225
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                                                        Local Similarity tes 5; Conserv
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 153
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                            1 FSRYAR 6
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FSKYAR 158
                                                           Conservative
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                                                                        90.3%;
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Pred. No.
                                                         1; Mismatches
                                                                        Score 28;
Pred. No.
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Pred. No. 3.8e+02;
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3e+02;
                                                                        3.9e+02;
                                                                                      DB 4;
                                                      0;
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                                                                                        Length 234;
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PILE REFERENCE: 9369-311
CURRENT APPLICATION NUMBER: US/10/987,454
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US 60/519,606
PRIOR PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US 60/579,733
PRIOR FILING DATE: 2004-06-16
NUMBER: OF SEQ ID NOS: 251
SOFTWARE: Patentin version 3.3
SEQ ID NO 122
LENGTH: 243
RESULT 45
US-10-183-687-160
(S-10-183-687-160)
; Sequence 160, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
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US-10-424-599-254640
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                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT ; ORGANISM: Arabidopsis thaliana US-10-987-454-122
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US-10-987-454-122
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APPLICANT: Kovalic David K
APPLICANT: Chou Yihua
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated in TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 254640
LENGTH: 239
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Best Local
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TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC
TITLE OF INVENTION: PLANTS
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ORGANISM: Glycine max
FEATURE:
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mes 5; Conservat
                                                                                                                                                               159
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5; Conserva
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83.3%;
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Pred. No. 4.1e+02;
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Pred. No. 4e+02;
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APPLICANT:

Allen, William B.

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APPLICANT: Shen, Bo
APPLICANT: Tarczynski, Mitchell C.
FITLE OF INVENTION: Alteration Of Oil Traits In Plants
FILE REFERENCE: BB1458 US NA
CURRENT APPLICATION NUMBER: US/10/183,687
CURRENT FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: 60/301,913
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 532
SOFTWARE: Microsoft Office 97
SEQ ID NO 160
LENGTH: 244
TYPE: PRT
ORGANISM: Zea mays
US-10-183-687-160
RESULT 47
US-10-437-963-133297
; Sequence 133297, Application US/10437963
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US-10-425-114-54567
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APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 54567
LENGTH: 256
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Glycine max
FEATURE:
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                                                                                         174 FSKYAR 179
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Oliveira, Igor Cunha
Sakai, Hajime
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Harvell, Leslie T.
Jones, Todd
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Klein, Ted
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                                                                                                                                                                  Conservative
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                                                                                                                                                                               90.3%;
                                                                                                                                                                1; Mismatches
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Pred. No. 4.3e+02;
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RESULT 49
US-10-987-454-128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-987-454-127
Sequence 127, Application US/10987454
Publication No. US20050172359A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-437-963-133297
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LENGTH: 285
                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.3
SEQ ID NO 127
LENCTH: 301
TYPE: PRT
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                           Matches
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                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/987,454
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US 60/519,606
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US 60/579,733
PRIOR FILING DATE: 2004-06-16
NUMBER OF SEQ ID NOS: 251
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APPLICANT: Moloney, Maurice
APPLICANT: Moloney, Maurice
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 9369-311
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APPLICANT: Kovalic, David K.
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ORGANISM: Oryza sativa
FEATURE:
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Zhou, Yihua
Cao, Yongwei
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Wu, Wei
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Barbazuk, Brad
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Pred. No. 4.8e+02;
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Sequence 128, Application US/10987454
Publication No. US20050172359A1
GENERAL INFORMATION:
APPLICANT: Reid, Alexandra
APPLICANT: Moloney, Maurice

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TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC; TITLE OF INVENTION: PLANTS; FILE REFERENCE: 9369-311
CURRENT APPLICATION NUMBER: US/10/987,454
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US 60/519,606
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2004-06-16
PRIOR FILING DATE: 2004-06-16
PRIOR FILING DATE: 2004-06-16
VOUNBER OF SEQ ID NOS: 251
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 128
LENGTH: 301
TYPE: PRT
CORGANISM: Hordeum vulgare
US-10-987-454-128
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Publication No. US20050196754A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790C1P3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/549,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 37522
LENGTH: 301
TYPE: PRI
TY
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; FEATURE:
; FEATURE:
; INAME/KEY: misc_feature
; LOCATION: (1)...(301)
; OTHER INFORMATION: Xaa = X or * as defined in Table
US-10-450-763-37522
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Matches 5; Conservative
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| MMC_Celerra_SIDS3/ptcodata/2/pubpaa/PCT_NEW_PUB.pep:*
| MMC_Celerra_SIDS3/ptcodata/2/pubpaa/US10_NEW_PUB.pep:*
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US-11-105-233-53

Sequence 53, Application US/11105233

Publication No. US20060134653A1

GENERAL INFORMATION:
APPLICANT: Thiagalingam et al
TITLE OF INVENTION: Differential Expression of Ger
TITLE OF INVENTION: Tumors
FILE REFERENCE: 1657/2001
CURRENT APPLICATION NUMBER: US/11/105,233
CURRENT FILING DATE: 2005-04-13

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SEQ ID NO 53
LENGTH: 174
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; TYPE: PRT
; ORGANISM: Homo s
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 RESULT 2
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; LOCATION: (1)..(240)
; OTHER INFORMATION: Ceres Seq. ID no. 13619980
US-11-056-355B-106575
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US-11-056-355B-106575
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                                                                                                                   US-11-056-355B-117814
                                                                                                                                        RESULT 4
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Best Local Similarity bo...
Thes 5; Conservative
                                                         Sequence 117814, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 106575
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APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590FUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
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                  APPLICANT: Brover, Vyacheslav APPLICANT: Alexandrov, Nicko:
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ORCANISM: Triticum aestivum
FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(225)
OTHER INFORMATION: Ceres Seq. ID no. 12614812
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: prt
ORGANISM: Arabidopsis thaliana
FEATURE:
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|156 FSKYAR 161
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    Mismatches

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APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
FTILE OF INVENTION: Sequence Determined DNA Fragments and
FTILE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 106574
LENGTH: 243
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; LCCATION: (11)..(243)
; OTHER INFORMATION: Ceres Seq.
US-11-056-355B-106574
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; OTHER INFORMATION: Ceres Seq. ID no. 13619980
US-11-056-355B-117814
                                                                                                                                                                   US-11-056-355B-117813; Sequence 117813, Application US/11056355B; Publication No. US20060150283A1
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Best Local S
Matches 5
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
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PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
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NAME/KEY: peptide
LOCATION: (1)..(2
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ORGANISM: Arabidopsis thaliana
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5; Conserv
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   no.
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38;
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; LOCATION: (1)..(255)
; OTHER INFORMATION: Ceres Seq. ID
US-11-056-355B-106573
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NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 117813
                                                                                                                                                                                                                        Sequence 117812, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
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LENGTH: 255
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Best Local Similarity
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SEQ ID NO 117812
LENGTH: 255
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Matches 5; Conserv
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                                                                                       APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR ETILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
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                                  PRIOR APPLICATION NUMBER: 60/544,190 PRIOR FILING DATE: 2004-02-13 NUMBER OF SEQ ID NOS: 119966
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LOCATION: (1)..(243)
OTHER INFORMATION: C
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ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
FEATURE:
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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39;
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Sequence 68810, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
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; LOCATION: (1)..(255)
; OTHER INFORMATION: C
US-11-056-355B-117812
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TYPE: prt ORGANISM: Triticum aestivum Pragmune: Triticum aestivum
                                                                                                                                             Sequence 68809, Application US/11056355B

Publication No. US20060150283A1

GENERAL INFORMATION:

APPLICANT: Brover Vyacheslav

APPLICANT: Alexandrov, Nickolai

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Polypeptides Encoded Thereby

FILE REFERENCE: 2750-1590PUS2

CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT FILING DATE: 2004-02-14

PRIOR APPLICATION NUMBER: 60/544,190

PRIOR FILING DATE: 2004-02-13

NUMBER OF SEQ ID NOS: 119966
                                                                                                               SEQ ID NO 68809
LENGTH: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local 9
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NAME/KEY: peptide
LOCATION: (1)..(301)
OTHER INFORMATION: Ceres Seq. ID no. 12614811
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NAME/KEY: peptide
LOCATION: (1)..(348)
OTHER INFORMATION: Ceres Seq.
                                                                      TYPE: prt
ORGANISM: Triticum aestivum
                                                            FEATURE:
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Pred. No.
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   ID no.
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US-10-953-349-9971
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US-10-449-902-37988
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 9971
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GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
PILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION UNMEER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9971, Application US/10953349
Publication No. US20060107345A1
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Best Local Similarity
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Best Local
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Poundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                                                   TYPE: PRT
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TYPE: PRT
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83.3%;
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Pred. No. 86;
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RESULT 15
US-10-953-349-2962
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US-10-953-349-2963
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US-10-953-349-7495
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 7495
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GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 2963
LENGTH: 209
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 2962
LENGTH: 216
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                                                                       APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DI
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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TYPE: PRT
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Pred. No.
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ORGANISM: Arabidopsis thaliana

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RESULT 16
US-10-953-349-7494
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION UMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 9130
LENGTH: 290
Sequence 202, Application US/11174307B Publication No. US20060143729A1 GENERAL INFORMATION:
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERBY
TITLE OF INVENTION: SEQUENCE-DETERBY
TITLE OF INVENTION: SEQUENCE-DETERBY
TITLE OF INVENTION: SEQUENCE-DETERBY
TITLE OF INVENTION SEQUENCE-DETERBY
TITLE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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TYPE: PRT
ORGANISM: Arabidopsis thaliana
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Pred. No.
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Pred. No.
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Pred. No.
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59;
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US-10-449-902-56777

Sequence 56777, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Instit
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science
APPLICANT: Foundation for Advancement of International Science
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT APPLICATION NUMBER: US/10/449,902
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2003-05-30
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Best Local S
Matches 5
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TITLE OF INVENTION: NUCLECTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
TITLE OF INVENTION: USEPTL FOR MODIFYING PLANT CHARACTERISTICS
FILE REFERENCE: 2750-1601PUS2
CURRENT APPLICATION NUMBER: US/11/174,307B
CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: 60/583,671
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,781
PRIOR APPLICATION NUMBER: 60/583,781
PRIOR APPLICATION NUMBER: 60/583,781
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,781
PRIOR FILING DATE: 2004-06-30
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PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 5544
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ORGANISM: Arabidopsis thaliana
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OTHER INFORMATION:
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OTHER INFORMATION: PFam
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OTHER INFORMATION: PFam Name: RRM_1; PFam Description: RNA recognition motif.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            59
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83.3%;
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US-10-449-902-34829
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US-10-953-349-21500
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US-10-449-902-56777
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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Publication No. US20060123505A1
GENERAL INFORMATION:
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SEQ ID NO 21500
LENGTH: 334
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 56777
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                                                                                                            SOFTWARE: PatentIn Ver. SEQ ID NO 34829
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Best Local :
   Query Match
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PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                    TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF FILE REFERENCE: MOA-A0205Y1-US CURRENT APPLICATION NUMBER: US/10/449,902 CURRENT FILING DATE: 2003-05-29
                                                                                                                                                                                                                                                                                                           APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
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CURRENT FILING DATE: 2004-09-30
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                                                     TYPE: PRT
ORGANISM: Oryza sativa
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                                                                            LENGTH: 338
TYPE: PRT
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TYPE: PRT
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83.3%;
     87.1%; Score 27;
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Pred. No.
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RESULT 24
US-10-449-902-45028
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 21499
LENGTH: 353
TYPE: PRT
                                                                                                                                              ; ORGANISM: Oryza sativa 
US-10-449-902-33374
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US-10-953-349-21499
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
                                                                      Matches
                                                                                         Query Match
Best Local
                                                                                                                                                                                                  SEQ ID NO 33374
LENGTH: 374
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PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
                                                                      Local Similarity
les 5; Conserv
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les 5; Conserv
345
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                                 1 FSRYAR 6
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FORYAR 350
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Pred. No.
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                                                                                       Score 27; DB 6;
Pred. No. 1e+02;
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96;
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US-11-330-403-7004
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Best Local Similarity
Watches 5; Conserve
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; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45028
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APPLICANT: Abad, Mark S.

TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(5529)B

CURRENT APPLICATION NUMBER: US/11/330,403

CURRENT FILING DATE: 2006-01-12

NUMBER OF SEQ ID NOS: 19250

SEQ ID NO 7004

LENGTH: 478
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Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                              Sequence 7004, Application US/11330403 Publication No. US20060159563A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILLING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Glycine max
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83.3%;
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US-11-353-390A-7
Sequence 7, Application US/11353390A
Publication No. US20060185036A1
Publication No. US20060185036A1
GENERAL INFORMATION:
APPLICANT: Sticklen, Masomeh B
APPLICANT: Magbool, Shahina B
APPLICANT: Dale, Bruce E
TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULASE WHICH
TITLE OF INVENTION: DEGRADE LIGNIN AND CELLULOSE TO FERMENTABLE SUGARS
FILE REFERENCE: MSU 4.1-806
CURRENT FILING DATE: 2006-02-14
PRIOR APPLICATION NUMBER: US 60/242,408
PRIOR FILING DATE: 2000-10-20
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
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Best Local
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TITLE OF INVENTION: TRANSCENIC PLANTS CONTAINING LIGNINASE AND CELLULASE WHICH
TITLE OF INVENTION: DEGRADE LIGNIN AND CELLULOSE TO FERMENTABLE SUGARS
FILE REFERENCE: MSU 4.1-814
CURRENT APPLICATION NUMBER: US/11/399,675
CURRENT FILING DATE: 2006-04-06
PRIOR APPLICATION NUMBER: US 60/242,408
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2001-10-18
PRIOR FILING DATE: 2001-10-18
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APPLICANT: Maqbool, Shahina B
APPLICANT: Dale, Bruce E
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NAME/KEY: misc_feature
LOCATION: (316)...(316)
OTHER INFORMATION: The
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LOCATION: (113)..(113)
OTHER_INFORMATION: The
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LOCATION: (148)..(148)
OTHER INFORMATION: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Actinomyces naeslundii
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83.3%;
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Pred. No. 1.3e+02;
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US-11-354-310A-7
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LENGTH: 488
TYPE: PRT
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Best Local Similarity 83.3
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                                          Query Match
Best Local (
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                            Matches
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CURRENT APPLICATION NUMBER: US/11/354,310A
CURRENT FILING DATE: 2006-02-14
PRIOR APPLICATION NUMBER: US 60/242,408
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sticklen, Masomeh B
APPLICANT: Magbool, Shahina B
APPLICANT: Dale, Bruce E
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                                                                                                NAME/KEY: misc feature LOCATION: (316)...(316) OTHER INFORMATION: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Actinomyces naeslundii
FEATURE:
NAME/KEY: misc_feature
LOCATION: (113)...(113)
OTHER INFORMATION: The 'Xaa' at
                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (113)..(113)
                                                                                                                                                                                                                                                                      ORGANISM: Actinomyces naeslundii
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LOCATION: (148)..(148)
OTHER INFORMATION: The
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LOCATION: (148)..(148)
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TYPE: PRT
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                           Similarity 5; Conserv
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                                           Score 27; DB 7;
Pred. No. 1.3e+02;
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Pred. No. 1.3e+02
0; Mismatches
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CURRENT APPLICATION NUMBER: US/11/174,307B
CURRENT FILLING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: 60/583,671
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,781
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,651
PRIOR APPLICATION NUMBER: 60/583,651
PRIOR APPLICATION NUMBER: 60/583,651
PRIOR APPLICATION NUMBER: 60/583,651
PRIOR APPLICATION NUMBER: 50/583,651
PRIOR APPLICATION NUMBER: 50/583,651
PRIOR APPLICATION NUMBER: 50/583,651
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 5544
SEQ ID NO 4272
LENGTH: 541
RESULT 31
US-10-449-902-33781
; Sequence 33781, Application US/10449902
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                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: GI Number: 42522036; NR Description: Gene product i OTHER INFORMATION: ubiquinone production. [Bdellovibric bacteriovorus ; OTHER INFORMATION: >gi[39574567|emb|CAE78409.1| Gene product involved US-11-174-307B-4272
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Best Local
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TITLE OF INVENTION: NUCLECTIES SEQUENCES AND POLYPEPTIDES ENCODED
TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
FILE REFERENCE: 2750-1601PUS2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: GI Number: 45657281; NR Description: ubiquinone biosynthesis OTHER INFORMATION: protein [Leptospira interrogans serovar Copenhageni str. Fioo OTHER INFORMATION: L1-130] >gi | 45600519 | gb | AAS70004.1 | ubiquinone biosynthesis |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: GI Number: 50935257; NR Description: ABC1 family protein OTHER INFORMATION: kinase-like protein [Oryza sativa (japonica cultivar-group)] OTHER INFORMATION: >gi|23617237|dbj|BAC20904.1| ABC1 family protein kinase-like
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83.3%;
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Pred. No. 1.5e+02;
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Sequence 451, Application US/11337300
Publication No. US20060121580A1
GENERAL INFORMATION:
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US-11-056-355B-581
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GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nicko
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SEQ ID NO 33781
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APPLICANT: Bio-oriented Technology Research Advancement Institut
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
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PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
                    APPLICANT: Crucell Holland B.V. APPLICANT: ter Meulen, Jan H.
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NAME/KEY: peptide
LOCATION: (1)..(109)
OTHER INFORMATION: Ceres Seq. ID
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TYPE: PRT
ORGANISM: Oryza sativa
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ORGANISM: Zea mays subsp. mays
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nes 5; Conserv
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ter Meulen, Jan H.
De Kruif, Cornelis A.
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83.3%;
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Pred. No.
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Pred. No.
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TITLE OF INVENTION: Binding molecules against SARS-coronavirus and uses thereof; FILE REFERENCE: 0091 WO 00 ORD; CURRENT APPLICATION NUMBER: US/11/337,300; CURRENT FILING DATE: 2006-01-20; NUMBER OF SEQ ID NOS: 478
SOFTWARE: PatentIn version 3.1
SEQ ID NO 451
LENGTH: 170
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US-10-449-902-31883
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Best Local S
Matches
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Best Local Similarity
Matches 5; Conserv
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SEQ ID NO 31883
LENGTH: 217
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-30369
PRIOR FILLING DATE: 2002-05-30
PRIOR FILLING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
NUMBER OF SEQ ID NOS: 56791
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Publication No. US20060123505A1
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590FUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
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TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
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100.0%; Pred. No.
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1e+02;
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SEQ ID NO 286
LENGTH: 256
TYPE: PRT
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LENGTH: 219
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Matches 5; Conserv
                                                 APPLICANT: De Kruif, Cornelis A.
APPLICANT: Van den Brink, Edward N.
APPLICANT: Goudsmit, Jaap
TITLE OP INVENTION: Binding molecules against SARS-coronavirus and uses thereof
FILE REFERENCE: 0091 WO 00 ORD
CURRENT APPLICATION NUMBER: US/11/337,300
CURRENT FILING DATE: 2006-01-20
NUMBER OF SEQ ID NOS: 478
SOFTWARE: PatentIn version 3.1
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TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590FUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
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OTHER INFORMATION: Ceres Seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: peptide
LOCATION: (1)..(219)
OTHER INFORMATION: Ceres Seq. ID no. 12566294
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ORGANISM: Zea mays subsp. mays
FEATURE:
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De Kruif, Cornelis A.
                                                                                                                                                                                                                                                                                           Application US/11337300 to. US20060121580A1
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100.0%; Pred. No. 1e+02;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.9%; Score 26; DB 7; 100.0%; Pred. No. 1e+02;
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; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30299
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-30299
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; TYPE: PRT; ORGANISM: Oryza sativa
US-10-449-902-31725
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US-10-449-902-30299
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                                                                 SOFTWARE: PatentIn Ver.
SEQ ID NO 31725
LENGTH: 271
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Matches
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT APPLICATION NUMBER: US/202-203269
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-105-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR PILING DATE: 2002-12-11
NUMBER: SCC 17 NOC: 56701
                                                                                                                                                                                                                                                                                                                  APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
                                                                                                                                   PRIOR APPLICATION NUMBER: JP 2002-383870 PRIOR FILING DATE: 2002-12-11 NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                                   FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 2002-203269 PRIOR FILING DATE: 2002-05-30
                                                LENGTH:
TYPE: PR
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100.0%; Pred. No. 1.3e+(
ive 0; Mismatches
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Pred. No. 1.2e+02;
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Best Local Similarity

Query Match

Length 271;

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US-10-449-902-32135
                                                                                                                         ; ORGANISM: Oryza sativa
US-10-449-902-51604
          Query Match
Best Local Similarity luv.
Thes 5; Conservative
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Publication No. US20060123505A1
GENERAL INFORMATION:
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SEQ ID NO 51604
LENGTH: 271
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SEQ ID NO 32135
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Best Local Similarity
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER: OF SEQ. ID NOS: 56791
NUMBER: OF SEQ. ID NOS: 56791
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APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
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PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
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APPLICANT: Bio-oriented Technology Research Advancement
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100.0%; Pred. No. 1.3e+02;
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100.0%; Pred. No.
                                      83.9%; Score 26; DB
100.0%; Pred. No. 1.3
cive 0; Mismatches
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5. 1.3e+02;
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RESULT 42
US-11-056-355B-7374
; Sequence 7374, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 16849
LENGTH: 271
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Matches 5; Conserv
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LENGTH: 271
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                                                                     Matches
                                                                                                   Query Match
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APPLICANT: Alexandrov, Nickolii
ITTLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590FUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
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                                                                                                                                                     NAME/KEY: peptide
LOCATION: (1)..(271)
OTHER INFORMATION: Ceres Seq. ID no. 12566292
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NAME/KEY: peptide
LOCATION: (1)..(2
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ORGANISM: Zea mays subsp. mays
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ORGANISM: Zea mays subsp. mays
FEATURE:
                                                               Local Similarity hes 5; Conserv
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                                 1 FSRYA 5
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                                                                 Conservative
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100.0%;
                                                                   83.9%; Score 26; DB 7;
100.0%; Pred. No. 1.3e+Cive 0; Mismatches
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Pred. No.
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. 1.3e+02;
                                                                                      1.3e+02;
                                                                                                       Length 271;
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RESULT 44

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RESULT 46
US-11-330-403-19189
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; LENGTH: 334
; TYPE: PRT
; ORGANISM: Staphylococcus aureus subsp. aureus Mu50
US-11-330-403-9151
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US-11-330-403-9151
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APPLICANT: Abad, Mark S.
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                                                                                                                                                                     Sequence 19189, Application US/11330403
Publication No. US20060159563A1
GENERAL INFORMATION:
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Publication No. US20060159563A1
SEQ ID NO 19189
LENGTH: 334
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
RUMBER OF SEQ ID NOS: 119966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21[53629]8 CURRENT APPLICATION NUMBER: US/11/330,403 CURRENT FILING DATE: 2006-01-12 NUMBER OF SEQ ID NOS: 19250
                                                     CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
NUMBER OF SEQ ID NOS: 19250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brover, Vyacheslav APPLICANT: Alexandrov, Nickolai
                                                                                                             APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53629)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: peptide
LOCATION: (1)..(311)
OTHER INFORWATION: Ceres Seq. ID no. 12412611
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ORGANISM: Zea mays subsp. mays
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                83.9%;
Local Similarity 83.3%;
es 5; Conservative
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Query Match
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                                                  ; TYPE: PRT
; ORGANISM: Homo
US-11-359-554-3
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APPLICANT: Xiao, Yonghong
TITLE OF INVENTION: Regulation of Human Prostasin-Like
TITLE OF INVENTION: Serine Protease
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                                                                                                                     SOFTWARE: FastSEQ
SEQ ID NO 3
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Publication No. US20060154293A1
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Best Local Similarity
Query Match
Best Local Similarity
                                                                                                                                                      PRIOR APPLICATION NUMBER: US/10/311,591
PRIOR FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US 60/213,474
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/277,612
PRIOR PILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                           FILE REFERENCE: 004974.00929
CURRENT APPLICATION NUMBER: US/11/359,554
CURRENT FILING DATE: 2006-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/311,055
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CURRENT FILING DATE: 2006-04-14
PRIOR APPLICATION NUMBER: US/10/109,616
PRIOR FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHANNEL
TITLE OF INVENTION: ACTIVATING PROTEASE 1 (CAP1) GENE DISRUPTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: R-490
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                                                                                                    LENGTH: 343
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Pred. No. 1.
 Score 26;
Pred. No.
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Pred. No. 1.6e+02;
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1.6e+02;
 1.6e+02;
                  DB 7;
                  Length 343;
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Sequence 22, Application US/11333747A

Publication No. US20060160159A1

GENERAL INFORMATION:
APPLICANT: Handfield, Martin
APPLICANT: Hillman, Jeffrey
APPLICANT: Progulske-Fox, Ann
TITLE OF INVENTION: Identification of Actinobacillus actinomycetemcomitans
TITLE OF INVENTION: Antigens for Use in the Diagnosis, Treatment, and Monitoring
TITLE OF INVENTION: of Periodontal Diseases
FILE REFERENCE: WHHB01-662C
CURRENT APPLICATION NUMBER: US/11/333,747A
CURRENT FILING DATE: 2006-01-17
PRIOR APPLICATION NUMBER: US 09/995493
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: PCT/US02/37235
PRIOR FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 234
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
LENGTH: 365
TYPE: PAT
ORGANISM: Actinobacillus actinomycetemcomitans
US-11-333-747A-22
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, NAME/KEY: MISC FEATURE
; LOCATION: (1). (348)
; OTHER INFORMATION: conserved hypothetical
US-10-471-571A-4440
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US-10-471-571A-4440
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CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 4440
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publication No. US20060115490A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
                                                                      Query Match 83.9
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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TYPE: PRT
ORGANISM: Staphylococcus aureus
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278 FSRYA 282
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                                                                          83.9%; Score 26; DB 7; Length 365;
100.0%; Pred. No. 1.7e+02;
ative 0; Mismatches 0; Indels
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Pred. No. 1.6e+02;
0; Mismatches 1
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Search completed: August 29, 2006, 11:29:12 Job time: 4.75248 secs

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Perfect score:
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                                                                                                                                                                                                                                                                                                   motoneuronotrophic; motor neuron; Nootropic; Neuroprotective; Vulnerary; Neuropeptide-Agonist; axon degeneration; muscle reinnervation; peripheral nerve; neurodegenerative; wound healing.
                                                                                                                                                                                             21-OCT-2004
                                                                                                                                                                                                               ADQ90197;
WPI; 2004-562147/54
                 Chau RMW,
                                                    21-JAN-2003; 2003US-0441772P
                                                                     21-JAN-2004;
                                                                                       05-AUG-2004
                                                                                                        WO2004065410-A2
                                                                                                                         Unidentified
                                                                                                                                                                           WMLSAFS
                                                                                                                                                                                                                               ADQ90197 standard;
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                                                                                                                                                                           motoneuronotrophic
                                                                                                                                                                                                                             peptide;
                                                                                                                                                                                            entry)
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AEB37487

AEB3674867

AAB3674067

AAG18090

AAG43063

AAG2002510

AEF29059

AAG30769

AAB990870

ABB971511

ADQ74828

ADD74828

ADD74828

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AAG30794

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AAG30794

AAG401808

ADD725091

AAG401808

ADD725091

AAG20782

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ADD725091

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Aeb37487 L. pneumo
Aeb36748 L. pneumo
Aeb36748 L. pneumo
Aeg20022 Arabidops
Aag218090 Arabidops
Aag18090 Arabidops
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Aag30769 Arabidops
Abb84448 Siah-rela
Abp71511 Arabidops
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Aabb84458 Siah-rela
Abb81458 Siah-rela
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Abb47176 Listeria
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RESULT 2
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ID ADQ90200
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                                                                                   The present invention relates to motoneuronotrophic factor peptide analogue, where the peptide analogue enhances the viability of motor neurons. The methods and compositions of the present invention are useful for promoting motor neuron viability and axon degeneration, target muscle reinnervation, treating peripheral nerve injuries, treating neurodegenerative disease and in wound healing. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                     New motoneuronotrophic factor peptide analogue enhancing the viability motor neurons, useful for target muscle reinnervation, treating peripheral nerve injuries or neurodegenerative diseases and in wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peripheral nerve;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   motoneuronotrophic; motor neuron; Nootropic; Neuroprotective; Vulnerary; Neuropeptide Agonist; axon degeneration; muscle reinnervation;
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                                                                                                                                                                                                                                                                                                       Claim
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                                                              represents a MNTF motoneuronotrophic factor peptide analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-) GENERVON BIOPHARMACEUTICALS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RMW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ist; axon degeneration; muscle reinnervation;
neurodegenerative; wound healing.
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Pred. No.
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Sequence 13 AA;

RESULT 4
AA029914
ID AA02

AAO29914 standard; protein; 33 AA

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RESULT 3
AAWS9046
ID AAWS
XX AAWS
AC AAWS
XX Huma
XX Huma
XX Moto
KW Moto
CO 2-4
PR 12-4
PR 12
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Matches 7
                                                                                                                                                                                                                                                              This sequence, represents a fragment of a novel human motoneurotrophic factor, MNTF1-F6. Such factors are used to promote regeneration of the axon of a motoneurone, to diagnose and treat motoneurone disease in a mammal or to accelerate wound healing whilst concomitantly minimising or inhibiting scar tissue and/or reloid formation in an area associated with a wound. For promoting axonal regeneration, the polypeptide is administered at a concentration of 5 ng-50 mg, whereas for inhibiting hereditary motoneurone disease, the dosage is 5-100 (especially 30-50) ng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-1996;
15-NOV-1996;
12-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Motoneurotrophic factor MNTF1-F3 and MNTF1-F6 - useful for motoneuron regeneration, diagnosing or treating motoneuron disease and to acceles wound healing without scar formation.
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                                                                                                                                                                                            Sequence 33
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7; Conserv
                                               1 WMLSAFS 7
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                                                                                                                                                                                               AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnose; treatment; disease; wound healing; scar
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                                                                                                Conservative
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96US-00751225.
97US-00928862.
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Pred. No.
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RESULT 5
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AC ADQ9
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DT 21-C
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KW MOTO
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                              peripheral nerve injuries, musculoskeletal disorders, spinal cord injuries, head injuries, strokes, neuromuscular degenerative diseases, amyotrophic lateral sclerosis, spinal muscular atrophy, peripheral neuropathy, diabetic peripheral neuropathy, peripheral neuropathy resulting from AIDS or radiation therapy for cancer, multiple sclerosis, muscular dystrophy, inhibition of scar formation, myasthenia gravis and sensory neuronal function disorders. The present sequence is human MNTF1-F6 protein used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peripheral nerve injury; musculoskeretat utrocker; nootropic; head injury; stroke; neuromuscular degenerative disease; nootropic; head injury; stroke; neuromuscular degenerative disease; nootropic; amyotrophic lateral sclerosis; peripheral neuropathy; neuroprotective; muscular dystrophy; AIDS; spinal muscular atrophy; multiple sclerosis; muscular dystrophy; AIDS; sensory neuronal function disorder; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for promoting the survival, growth, proliferation or maintenance of mammalian neurons by administering motoneuronotrophic factors (MNTF). The method is useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Promoting the survival, growth, proliferation or maintenance of mammalian neurons by administering motoneuronotrophic factors, useful for treating musculoskeletal and neurodegenerative disorders and spinal cord injuries.
motoneuronotrophic; motor neuron; Nootropic; Neuroprotective; Vulnerary; Neuropeptide-Agonist; axon degeneration; muscle reinnervation;
                                                   MNTF1-F6 33 mer motoneuronotrophic factor peptide analogue.
                                                                                       21-OCT-2004
                                                                                                                                                        ADQ90195 standard; peptide; 33
                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 2B; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chau RMW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; motoneuronotrophic factor; MNTF; therapy; radiation therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
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DB; AAL60573.
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                                                                                     (first entry)
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100.0%; Pr
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Pred. No. 2.8;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to motoneuronotrophic factor peptide analogue, where the peptide analogue enhances the viability of motor neurons. The methods and compositions of the present invention are useful for promoting motor neuron viability and axon degeneration, target muscle reinnervation, treating peripheral nerve injuries, treating neurodegenerative disease and in wound healing. The present sequence represents MNTF1-F6 33 mer motoneuronotrophic factor peptide analogue.
                                                                                                                                                           23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 16893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB63367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New motoneuronotrophic factor peptide analogue enhancing the viability motor neurons, useful for target muscle reinnervation, treating peripheral nerve injuries or neurodegenerative diseases and in wound
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                                                   Venter JC,
                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                              27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
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                                                   Adams M,
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2000US-00614150
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Pred. No.
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2.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL040-ABL16175) and the encoded proteins (ABE5737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 16893; 21pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes
            The invention describes a method of identifying compounds that inhibit the activity of, or that interact with a protein essential for Drosophila larval viability comprising expressing in a recombinant host a DNA molecule to produce a protein essential for larval viability. The method
                                                                                                                 Identifying inhibitors of activity of proteins essential for Drosophila larval viability comprises expressing in a host a protein essential for larval activity and identifying compounds that inhibit or interact with
                                                                                                                                                                                                              Stam L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Larval viability associated
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                                                                           Claim 1; Page 120-126; 169pp; English
                                                                                                                                                                                                                                         (SYGN
                                                                                                                                                                                                                                                                                             18-JAN-2002; 2002WO-US001568
                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
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)B; ABS51396.
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Drosophila and
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                                                                                                                                                                                                                                                                                                                                                                                                                    ; insecticidal activity; maize; wheat;
millet; turf; cotton; sugarcane; suga
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Pred. No. 7.7e-
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Niknejad A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identified are useful as insecticides in crops such as maize, wheat, oats, rye, sorghum, rice, barley, millet, turf, cotton, sugarcane, suppert, oilseed rape, soybeans, vegetable crops and fruits. This is the amino acid sequence of a fruit fly larval viability associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1760 AA;
                                                                                                                                                                                                                                                                       08-AUG-2003; 2003US-0493599P
08-AUG-2003; 2003US-0493836P
08-AUG-2003; 2003US-0493867P
08-AUG-2003; 2003US-0493985P
                                                                                                                                                                                                                                                                                                                                                                                                                                                       emesis; constipation; diarrhea; cardiovascular disease; immune dendocrine disease; gastrointestinal disease; metabolic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cardiovascular disorder
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                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                               Antidiarrheic;
                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatotropic; Litholytic; Immunosuppressive; Gastrointestinal-Gen Antiinflammatory; Antidiabetic; Dermatological; Antiemetic; Laxat:
                                                                                                                                                                                                                                                                                                                                                                                                                                             dermatological disease; musculoskeletal disease; Cardiant; Vasotropic;
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(NOVS ) NOVARTIS A
(NOVS ) NOVARTIS PI
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se K, Saudrais
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7.7e+02;
                                                                                                                                                                                                Cusin I, Mahe C, Scherer A,
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The invention relates to a method of screening and/or diagnosing a cardiovascular disorder (CD) in a subject which comprises detecting and/or quantifying the level of a polypeptide in a biological sample from the subject and comparing the level to that of control sample. The method is useful for screening, diagnosing and treating coronary artery disease, biliary cirrhosis, gallstones, celiac disease, irritable bowel syndrome, diabetes, scleroderma, nausea, vomiting, constipation and diarrhea. The method is rapid and efficient. The present sequence represents a cardiovascular disorder plasma protein tryptic fragment.

Screening and/or diagnosing cardiovascular disorder in subject involves detecting and/or quantifying level of polypeptide in biological sample from subject and comparing with control sample.

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                                                                                     CC lubricating molety and has a polypeptide sequence comprising 1-76 repeats CC of a motif having at least 50% identity to the sequence KEPAPTT CC (AAB29774). The invention also relates to a nucleic acid encoding a human CC MSF-derived tribonectin; a biocompatible composition comprising a human CC tribonectin for inhibiting tissue adhesion formation; and a method of CC diagnosing osteoarthritis or a predisposition to osteoarthritis by CC measuring the amount of MSF or its fragment in a biological sample of a CC indicates the presence of or predisposition to developing osteoarthritis. CC indicates the presence of or predisposition to developing osteoarthritis. CC indicates the presence of or predisposition to developing osteoarthritis. CC osteoarthritis, where they may be used for lubricating mammalian joints, CC such as articulating joints of humans, dogs or horses. The tribonectin, CC when formulated as a membrane, foam, gel or fibre, is useful for CC inhibiting adhesion between two surfaces such as the injured tissues of a CC mammal, where the injury is caused by a surgical insertion or trauma, or can artificial device e.g., an orthopaedic implant. In particular, one of the surfaces is pericardial tissue. DNA encoding a tribonectin may be considered as the present sequence represents a fragment of a human MSF-derived tribonectin sequence represents a fragment of a human MSF-derived tribonectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human tribonectin; MSF; megakaryocyte stimulating factor; alternative splicing; joint boundary lubricant; O-linked oligosaccharide; osteoarthritis; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritic; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel tribonectin polypeptide useful as lubricant for treating osteoarthritis, comprises O-linked lubricating moiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jay GD;
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-024673/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The tribonectin has at least one O-linked oligosaccharide
                                                                       in gene ther
MSF-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         υ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Matches 6; Conserv
                                                           dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polymuclectides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polymuclectides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions; graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in Example of activities include: cytostatic; proliferative, vulnerary, immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antirheumatic; antirheumatic; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 2133; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing \mathbf{e}.\mathbf{g}. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-587533/55.
N-PSDB; AAC78216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC77607 to AAC78448 encode the human cancer associated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                     present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM
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RESULT 11
AAO18834
ID AAO18834
XX AAO18
XX AAO18
XX AAO18
XX SZP;
KW SZP;
KW degen
KW chond
KW immun
XX Homo
X
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Best Local
  Matches
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                                                                                                                                              The present invention provides the protein and coding sequences of human superficial zone protein (SZP). The protein is involved in the lubrication of joints, and the sequences can be used in the treatment of degenerative joint conditions or to delay symptoms of a degenerative joint condition, e.g. osteoarthritis, rheumatoid arthritis, gout, psoriatic arthritis, reactive arthritis, viral or post viral arthritis, spondylarthritis, juvenile arthritis, synovitis, tendontitis, systemic lupus erythematosus, CACP, osteoporosis or trauma. The present sequence is the protein encoded by the human 3' cartilage SZP cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New purified superficial zone protein (SZP) polypeptides, useful for treating degenerative joint conditions, e.g. osteoarthritis, rheumatoid arthritis, gout, spondylarthritis, synovitis, tendonitis, lupus, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         degenerative joint condition; arthritis; osteoporosis; trauma; CACP; chondroitin sulphate substitution consensus; antiarthritic; antirheumatic; osteopathic; antigout; antiinflammatory; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SZP; superficial zone protein; cartilage; lubrication; degenerative joint condition; arthritis; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3' cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-636585/68.
N-PSDB; AAL49079.
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                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hutchins JT, Dixon EP;
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Local Similarity
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     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             superficial zone protein coding sequence encoded protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                  86-87;
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                           86.8%;
                                                                                                                                                                                                                                                                                                                                                                                                               89pp; English.
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Pred. No.
  0
                           Score 33; DB 5;
Pred. No. 5.4e+02;
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     Mismatches
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                                                 Length 538;
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     Indels
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     Gaps
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811 WMLSPFS

WMLSAFS

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RESULT 12
AAB29778
ID AAB29
XX AAB29
XX AAB29
XX AAB29
XX AAB29
XX Human
XX Human
XX Homo
XX Homo
XX Homo
XX AAB29
XX AA
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                                                                                                                                                                              CC lubricating molety and has a polypeptide sequence comprising 1-76 repeats CC of a motif having at least 50% identity to the sequence KEPAPT CC (AAB29774). The invention also relates to a nucleic acid encoding a human CC MSF-derived tribonectin; a biocompatible composition comprising a human CC diagnosing osteoarthritis or a predisposition formation; and a method of CC diagnosing osteoarthritis or a predisposition to osteoarthritis by CC measuring the amount of MSF or its fragment in a biological sample of a CC indicates the presence of or predisposition to developing osteoarthritis. CC The tribonectin and DNA encoding it are useful in the treatment of CC such as articulating joints of humans, dogs or horses. The tribonectin, CC when formulated as a membrane, foam, gel or fibre, is useful for CC inhibiting adhesion between two surfaces such as the injured tissues of a CC mammal, where the injury is caused by a surgical insertion or trauma, or CC an artificial device e.g., an orthopaedic implant. In particular, one of the surfaces is pericardial tissue. DNA encoding a tribonectin may be used in gene therapy. The present sequence represents a substantial cc portion of a human MSF-derived tribonectin
                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human MSF-derived tribonectin.
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                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel tribonectin polypeptide useful as lubricant for treating osteoarthritis, comprises O-linked lubricating moiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-024673/03
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                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The tribonectin has at least one O-linked oligosaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
Similarity 6; Conserv
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                              86.8%;
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   0;
                              Score 33;
Pred. No.
          Mismatches
                                     9.3e+02;
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                                                                Length 902
   Indels
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RESULT 14
ADZ03664
ID ADZ03
XX
AC ADZ03
XX
DT 02-JU
DT 02-JU
XX
XX
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                                                                                                                                                                                                                 Matches
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Best Local (
                                                                                                                                                                                                                                                                                                The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% or 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, neurological concers. This sequence corresponds to a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JAN-2003; 2003JP-00102206.
09-MAY-2003; 2003JP-00131392.
  lubricin;
                          PRG4 - Lub:1
                                                 02-JUN-2005
                                                                          ADZ03664;
                                                                                                 ADZ03664 standard; protein; 981
                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 4874; 2449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JAN-2004; 2004EP-00001196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto
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                                                                                                                                                                700 WMLSPFS 706
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                                                                                                                                                                                      1 WMLSAFS
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                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                933 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                         of the invention.
antiarthritic; osteopathic; antirheumatic; cytostatic;
                        protein.
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                                                                                                                                                                                                                Conservative
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                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isono Y,
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                                                 entry)
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                                                                                                                                                                                                                           86.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          933
                                                                                                                                                                                                              <u>,,</u>
                                                                                                                                                                                                                          Score 33; DB 8; Pred. No. 9.7e+02;
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                                                                                                                                                                                                                                     Length 933;
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RESULT 15
ADZ03668
ID ADZ03
XX ADZ03
XX ADZ03
XX D2-JU
XX DPRG4-
XX Lubri
KW Cardi
KW neopl
XX neopl
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XX Neopl
XX Syntl
XX Syntl
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XX X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated lubricin protein. A lubricin containing composition is useful for treating a subject which involves administering same to a tissue (e.g. cartilage, synovium, meniscus, tendon, peritoneum, pericardium, or pleura (preferably cartilage)) of the subject (e.g. mouse, rat, cat, dog, horse or human (preferably human)). The above method further involves providing an anasthetic, antiinflammatory drug and antibiotic to the subject, aspirating fluid from the subject, washing tissue of the subject and imaging tissue of the subject. The protein is useful for treating osteoarthritis or rheumatoid subject. The protein is useful for treating osteoarthritis or rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arthritis, or as lubricants, anti-adhesive agent or intra articular supplements for synovial joints, meniscus, tendon, peritoneum, pericardium or pleura. An anti-lubricin antibody is useful for treating cancer e.g. synoviomas. The present sequence represents the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel recombinant lubricin useful for treating osteoarthritis or rheumatoid arthritis, or as lubricants, anti-adhesive agent or intra articular supplements for synovial joints, meniscus, tendon, peritoneum, pericardium or pleura.
                                                                                                                lubricin; antiarthritic; osteopathic; antirheumatic; cytostatic; cardiant; respiratory-gen.; osteoarthritis; rheumatoid arthritis neoplasm; musculoskeletal disease; immune disorder; inflammation
                                                                                                                                                                                                                     02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 981 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer e.g. synoviomas. The present sequence of the PRG4-Lub:1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; SEQ ID NO 7; 19pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2003; 2003US-0495741P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiant; respiratory-gen.; osteoarthritis; rheumatoid arthritis; neoplasm; musculoskeletal disease; immune disorder; inflammation.
                                                 WO2005016130-A2
                                                                                                                                                                                  PRG4-Lub:2 protein
                                                                                                                                                                                                                                                                                      ADZ03668 standard;
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                                                                                                                                                                                                                                                                                   protein; 1007
                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.8%;
85.7%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9;
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RESULT 16
ADZ03672
ID ADZ03
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AC ADZ03
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DT 02-JU
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Lubri
KW Lubri
KW cardi
KW neopl
XX
NOOE
PN WO200
XX
DT 24-PI
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PF 13-AL
XX
PR (AMHI
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PR WPI;
PR WPI;
PR WPI;
PR WPI;
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel recombinant lubricin useful for treating osteoarthritis or rheumatoid arthritis, or as lubricants, anti-adhesive agent or intra articular supplements for synovial joints, meniscus, tendon, peritoneum, pericardium or pleura.
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sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated lubricin protein. A lubricin containing composition is useful for treating a subject which involves
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                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                               02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1007 AA;
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                WPI; 2005-272808/28
                                                                                                          14-AUG-2003; 2003US-0495741P
                                                                                                                                          13-AUG-2004; 2004WO-US026508
                                                                                                                                                                       24-FEB-2005.
                                                                                                                                                                                                      WO2005016130-A2
                                                                                                                                                                                                                                                                   neoplasm;
                                                                                                                                                                                                                                                                                  lubricin; antiarthritic; osteopathic; antirheumatic; cytostatic;
cardiant; respiratory-gen.; osteoarthritis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                              PRG4-Lub:3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                            ADZ03672 standard;
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                                               Corcoran CJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                               entry)
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85.7%;
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Pred. No. 1e+0
0; Mismatches
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                                               BA,
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                                               Racie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1007;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated lubricin protein. A lubricin containing composition is useful for treating a subject which involves administering same to a tissue (e.g. cartilage, synovium, meniscus, tendon, peritoneum, pericardium, or pleura (preferably cartilage)) of the subject (e.g. mouse, rat, cat, dog, horse or human (preferably human)). The above method further involves providing an anasthetic, antiinflammatory drug and antibiotic to the subject, aspirating fluid from the subject, washing tissue of the subject, and imaging tissue of the subject. The protein is useful for treating osteoarthritis or rheumatoid arthritis, or as lubricants, anti-adhesive agent or intra articular supplements for synovial joints, meniscus, tendon, peritoneum, pericardium or pleura. An anti-lubricin antibody is useful for treating cancer e.g. synovicmas. The present sequence represents the amino acid sequence of the PRG4-Lub:3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel recombinant lubricin useful for treating osteoarthritis or rheumatoid arthritis, or as lubricants, anti-adhesive agent or intra articular supplements for synovial joints, meniscus, tendon, peritoneum,
                                                            rheumatoid arthritis, or as lubricants, articular supplements for synovial joint pericardium or pleura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1038 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; SEQ ID NO 15; 19pp; English
                              Claim 11; SEQ ID NO 19; 19pp; English
                                                                                            Novel recombinant lubricin useful for treating osteoarthritis or rheumatoid arthritis, or as lubricants, anti-adhesive agent or intra
                                                                                                                                        WPI; 2005-272808/28.
N-PSDB; ADZ03675.
                                                                                                                                                                                      Flannery CR,
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                                                                                                                                                                                                                                                                                 13-AUG-2004; 2004WO-US026508
                                                                                                                                                                                                                                                                                                                24-FEB-2005
                                                                                                                                                                                                                                                                                                                                             WO2005016130-A2
                                                                                                                                                                                                                                                                                                                                                                                                           neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                           cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRG4-Lub:4 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                       lubricin;
                                                                                                                                                                                                                     (AMHP ) WYETH
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6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         antiarthritic; osteopathic; antirheumatic; cytostatic;
respiratory-gen.; osteoarthritis; rheumatoid arthritis;
musculoskeletal disease; immune disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                       Corcoran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
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                                                                                                                                                                                       Freeman BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                              joints,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1e+03;
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                                                                                                                                                                                         Racie LA;
                                                                               meniscus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1038;
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                                                                              tendon, peritoneum
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invention relates to an isolated lubricin protein. A lubricin

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RESULT 18
ADZ03680
Matches
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        The invention relates to an isolated lubricin protein. A lubricin containing composition is useful for treating a subject which involves administering same to a tissue (e.g. cartilage, synovium, meniscus, tendon, peritoneum, pericardium, or pleura (preferably cartilage) of the subject (e.g. mouse, rat, cat, dog, horse or human (preferably human)). The above method further involves providing an anasthetic, antiinflammatory drug and antibiotic to the subject, aspirating fluid from the subject, washing tissue of the subject and imaging tissue of the subject. The protein is useful for treating osteoarthritis or rheumatoid subject. The protein is useful for treating osteoarthritis or rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 administering same to a tissue (e.g. cartilage, synovium, meniscus, tendon, peritoneum, pericardium, or pleura (preferably cartilage)) of the subject (e.g. mouse, rat, cat, dog, horse or human (preferably human)).
                                                                                                                                                                                                                                                                       Novel recombinant lubricin useful for treating osteoarthritis or rheumatoid arthritis, or as lubricants, anti-adhesive agent or is articular supplements for synovial joints, meniscus, tendon, per
                                                                                                                                                                                                                       Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2003; 2003US-0495741P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lubricin; antiarthritic; osteopathic; antirheumatic; cytostatic;
cardiant; respiratory-gen.; osteoarthritis; rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUN-2005
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arthritis,
                                                                                                                                                                                                                                                           pericardium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-2004; 2004WO-US026508
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DB; ADZ03679.
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                                                                                                                                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      respiratory-gen.; osteoarthriti: musculoskeletal disease; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                composition is useful
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                                                                                                                                                                                                                                                           or pleura.
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                                                                                                                                                                                                                   23; 19pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Freeman BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 9;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorder;
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                                                                                                                                                                                                                                                                           e agent or intra
tendon, peritoneum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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RESULT 19
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ID ADX677
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                                                                                                                                                                                                                                 New extracellular messengers and nucleic acids, useful for diagnosing, treating or preventing e.g. allergies, anemia, Crohn's disease, diabet mellitus, myasthenia gravis, osteoporosis, psoriasis, cancers or
                                                                                                                                                                                                                                                                                                                                                                                                                     Elliott VS
Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-AUG-2002; 2002US-0400810P.
19-SEP-2002; 2002US-0412197P.
04-OCT-2002; 2002US-0416004P.
08-NOV-2002; 2002US-0424862P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   muscular-gen.; antiarthritic; osteopathic; hepatotropic; antipsoriatic; virucide; fungicide; antiparasitic; protozoacide; antihelminthic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human extracellular messenger (EXMES) polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                         autoimmune thyroiditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                           vs,
                                                                                                                                                                                                                                                                                                                               ADK67916.
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, Emerling BM,
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                                                                                                                                                                ID
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                                                                                                                                                                NO 4; 165pp;
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85.7%;
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, Lindquist EA,
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Pred.
                                                                                                                                                                English
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                                                                                                                                                                                                                                                                                                                                                                                                                     chawla NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1100;
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                                                                                                                                                                                                                                                                                                                                                                                                     s JP;
K. Ramkumar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiallergic;
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The present sequence is that of novel human extracellular messenger (EXMES) Incyte ID NO: 7513017CD1 polypeptide. The protein shows homology to human megakaryocyte stimulating factor. The invention provides EXMES polynucleotides and polypeptides, as well as expression vectors, host cells, antibodies, agonists and antagonists, and methods for diagnosing, treating or preventing disorders associated with aberrant expression of

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ARESULT 20
AAM24322
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Best Local S
Matches 6
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17-JUL-2000;
03-AUG-2000;
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                          proteins from a variety of organisms, including human, dog, cat, ho cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
                                                                                                                                                                                                                                                                                                           Isolated polypeptide for treatment of antibodies and research use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200154477-A2
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                                                                                                                                                                                                                                                         Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-)
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                                                                                                                                                                                                 present invention provides the protein and coding sequences of novel
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                                                                                                                                                                                                                                                      20; Page 1198-1201; 1275pp; English.
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; 2000US-00617746.
; 2000US-00631451.
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85.7%;
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Pred. No. 1.3e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                   diagnostics, raising
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Matches 6
                                  The present sequence is that of novel human extracellular messenger (BXMES) Incyte ID NO: 7513018CD1 polypeptide. The protein shows homology to human megakaryocyte stimulating factor. The invention provides EXMES polynucleotides and polypeptides, as well as expression vectors, host cells, antibodies, agonists and antagonists, and methods for diagnosing, treating or preventing disorders associated with aberrant expression of EXMES, especially autoimmune and inflammatory disorders, cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiasthmatic; antiinflammatory; antidiabetic; neuroprotective; muscular-gen.; antiarthritic; osteopathic; hepatotropic; antipsoriatic; virucide; fungicide; antiparasitic; protozoacide; antihelminthic; cytostatic: gene therery
                                                                                                                                                          New extracellular messengers and nucleic acids, useful for diagnosing, treating or preventing e.g. allergies, anemia, Crohn's disease, diabet mellitus, myasthenia gravis, osteoporosis, psoriasis, cancers or autoimmune thyroiditis.
                                                                                                                                                                                                                                                                                                                                   02-AUG-2002; 2002US-0400810P.
19-SEP-2002; 2002US-0412197P.
04-OCT-2002; 2002US-0416004P.
08-NOV-2002; 2002US-0424862P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1299
           proliferative disorders and endocrine disorders, e.g. adult respiratory distress syndrome, allergy, anaemia, erythroblastosis foetalis, Crohn's
                                                                                                                                  Claim
                                                                                                                                                                                                                                                                      Richardson
                                                                                                                                                                                                                                                                                   Elliott VS,
                                                                                                                                                                                                                                                                                                                                                                                                30-JUL-2003; 2003WO-US024084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADK67912;
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                                                                                                                                                                                                                        N-PSDB;
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                                                                                                                                                                                                                      2004-157116/15.
)B; ADK67917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     extracellular
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6; Conserv
                                                                                                                                                                                                                                                                                                             INCYTE CORP
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                                                                                                                                  SEQ ID NO 5; 165pp; English.
                                                                                                                                                                                                                                                                        W.
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                                                                                                                                                                                                                                                                      Khare R, Ti
W, Emerling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          according
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Signal_peptide
/note= "Spans residues 1 to 18, 20,
according to identification method"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    messenger (EXMES) polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
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                                                                                                                                                                                                                                                                      UK, Swarnakar A,
, Lindquist EA,
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .4e+03;
                                                                                                                                                                                                                                                                        , Marquis
Chawla NK
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                                                                                                                                                                                                                                                                        NK,
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                                                                                                                                                                                                                                                                                     JP;
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                                                                                                                                                                                                                                                                         Ramkumar
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                                                                                                                                                                                    diabetes
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diabetes mellitus,

myasthenia gravis,

osteoarthritis,

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RESULT 22
ADK65819
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Best Local (
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                                          sequences, given in the specification, where the levels are indication the angiogenic index. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating cancoronary artery disease, myccardial ischemia or coronary arteriosclerosis. They can also be used in research, drug discovery forensic medicine involving angiogenesis. This sequence corresponds
                                                                                                                                                             The invention relates to a method of determining the angiogenic index of a tissue or cell sample comprising assessing, in a sample, the expression levels of one or more differentially-expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative of the angiogenic index. The methods and compositions of the present the angiogenic index. The methods and compositions of the present
                                                                                                                                                                                                                                                                                                                                                                                                     Determining the angiogenic index of a tissue or cell sample using expression levels of differentially expressed genes, useful for diagnosing or treating cancer, coronary artery disease, myocardial ischemia and/or arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2002; 2002US-00067482.
10-JUN-2002; 2002US-00164995.
16-AUG-2002; 2002US-0403649P.
03-JAN-2003; 2003US-0437746P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  their encoding polynucleotides for facilitating the drug discovery process, including determining of efficacy, dosage, toxicity and pharmacology, and for investigating the pathogenesis of diseases and medical conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parasitic, protozoal or helminthic infections, cancers, autoimmune thyroiditis, cretinism, Plummer's disease or thyroid carcinoma. thyroidments also provide methods for using the purified EXMESS and/or provide methods for using the purified EXMESS and provide methods for using the pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sun
                                                                                                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               angiogenesis inhibitor; angiogenesis stimulator; angiogenic index;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADK65819 standard; protein; 1320 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1311 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteoporosis, pancreatitis, psoriasis, viral, bacterial, fungal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ORIG-)
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f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-731502/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression; cancer; coronary artery disease; myocardial nary arteriosclerosis; forensic medicine.
                                                                                                                                                                                                                                                                                                                                                  23;
                        the differentially expressed proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 WMLSAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGENE TECHNOLOGIES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADK65818
                                                                                                                                                                                                                                                                                                                                               SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiant; vasotropic; antiarteriosclerotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kovacs
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                                                                                                                                                                                                                                                                                                                                            58; 296pp; English.
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85.7%;
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                           invention
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ny of 34 DNA
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                                                                                                                                        cancer,
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                                                                                                                                                                                                    of.
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RESULT 23
AAR26049
ID AAR26
XX ACC
ACC
AC AAR26
XX Megal
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XX Wegal
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FT Reg
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02-FEB-1993
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                                    New human mega-karyocyte stimulating factors - for treating immune deficiencies, cancer, exposure to radiation or drugs, bacterial and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
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                                                                                                            WPI; 1992-284660/34
                                                                                                                                                                                                                     18-JAN-1991;
10-SEP-1991;
                                                                                                                                                                                                                                                                               17-JAN-1992;
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                   infections, etc.
                                                                                                                                                                                                                                                                                                                                                   WO9213075-A1
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                                                                                                                                                                                   (GEMY ) GENETICS INST
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6; Conserv
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                                                                                                                                               Clark SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rte colony stimulating
proteolytic cleavage;
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91US-00757022
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.1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l= Exon_X
.1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l= Exon_IX
.1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l= Exon_VI
.1212
                                                                                                                                                                                     INC.
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                                                                                                                                                 Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Exon_III
                                                                                                                                                                                                                                                                                                                                                                                                                    Exon_XII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Exon_VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exon_V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exon_IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          factor; secretion signal;
adhesion; alternative spl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                               Hewick RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4e+03;
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                                                                                                                                                 Gesner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               meg-CSF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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Claim 1, 2 and 3; Fig 1; 87pp; English

III

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ARBSULT 24
AAB29773
ID AAB29
XX AAB29
XX AAB29
XX AB29
XX AB29
XX Human
XX Human
XX Human
XX Homo
XX OSLEO
XX O2-NO
XX WO200
XX W
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human MSF; megakaryocyte stimulating factor; tribonectin; alternative splicing; joint boundary lubricant; O-linked oligosaccharide; osteoarthrite; tribosupplementation; tissue adhesion inhibition; friction coefficient reduction; gene therapy; antiarthritic; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human megakaryocyte stimulating factor (MSF), SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB29773 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1404 AA;
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Novel tribonectin polypeptide useful as lubricant for treating osteoarthritis, comprises O-linked lubricating moiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-APR-2000; 2000WO-US010953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB29773;
                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                 (RHOD-) RHODE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1171 WMLSPFS 1177
                                                                                                                          2001-024673/03
DB; AAC81498.
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contains the initiating methionine, and encodes a classical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 WMLSAFS 7
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                                                                                                                                                                                                                                                                                                                                 ISLAND HOSPITAL LIFESPAN PARTNER
                                                                                                                                                                                                                                                                                                                                                                                                             99US-00298970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.8%;
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Pred. No. 1.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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1.5e+03;
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sequence is
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ARBSULT 25
AAB60568
ID AAB60
XX AAB60
XX AAB60
XX 27-AP
XX Human
XX Human
XX Homo
XX Ohrom
XX Homo
XX Ol-FE
XX 21-JU
PR 19-JU
PR 23-JU
PR 23-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       indicates the presence of or predisposition to developing osteoarthritis. The tribonectin and DNA encoding it are useful in the treatment of osteoarthritis, where they may be used for lubricating mammalian joints, such as articulating joints of humans, dogs or horses. The tribonectin, when formulated as a membrane, foam, gel or fibre, is useful for inhibiting adhesion between two surfaces such as the injured tissues of a mammal, where the injury is caused by a surgical insertion or trauma, or an artificial device e.g., an orthopaedic implant. In particular, one of the surfaces is pericardial tissue. DNA encoding a tribonectin may be used in gene therapy. The present sequence represents human MSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSF-derived tribonectin; a biocompatible composition comprising a human tribonectin for inhibiting tissue adhesion formation; and a method of diagnosing osteoarthritis or a predisposition to osteoarthritis by measuring the amount of MSF or its fragment in a biological sample of a mammal, wherein an increased amount of MSF compared to a control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene. The tribonectin has a polypeptide sequence comprising 1-76 repeats lubricating moiety and has a polypeptide sequence comprising 1-76 repeats of a motif having at least 50% identity to the sequence KEPAPTT (AAB29774). The invention also relates to a nucleic acid encoding a human (AAB29774).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human megakaryocyte stimulating factor (MSF, CACP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a human tribonectin which is a product of alternative splicing of the human MSF (megakaryocyte stimulating factor) gene. The tribonectin has at least one O-linked oligosaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 7; 47pp; English.
                                       New composition comprising the camptodactyly-arthropathy-coxa varapericarditis protein in combination with an anesthetic, useful for treating osteoarthritis, or as lubricants of tissue and joints.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; CACP protein; camptodactyly-arthropathy-coxa vara-pericarditis; MSF; megakaryocyte stimulating factor; synovial lubricant; chromosome 1q25-31; osteoarthritis; joint lubrication; osteopathic;
                                                                                                                                   WPI; 2001-182721/18.
                                                                                                                                                                                                                                                               23-JUL-1999; 99US-0145328P
19-JUL-2000; 2000US-00145328
                                                                                                                                                                                                                                                                                                                                  21-JUL-2000; 2000WO-US020002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                               Warman ML;
                                                                                                                                                                                                                        (UYCA-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                        CASE WESTERN RESERVE
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Pred. No. 1.5e+03;
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Example 1; Page; 34pp; English

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ADK65839
ID ADK65839
ID ADK65839
AC ADK65
XX ADK65
XX ADK65
XX Cytog
XX Cytog
XX Angic
XX Cytog
XX Angic
XX Coror
XX Angic
XX Coror
XX Homo
XX Homo
XX Homo
XX Homo
XX I1-Al
XX I1-Al
PR 11-JI
PR 11-JI
PR 10-JI
PR 03-JI
XX I1-Al
PR 03-JI
XX WPI;
XX UDete
PT claag
PT diag

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
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                                                                                                 Determining the angiogenic index of a tissue or cell sample using expression levels of differentially expressed genes, useful for diagnosing or treating cancer, coronary artery disease, myocardial ischemia and/or arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-FEB-2002; 2002US-00067482.
10-JUN-2002; 2002US-00164595.
16-AUG-2002; 2002US-0403649P.
03-JAN-2003; 2003US-0437746P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (ORIG-)
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                                     SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitor; angiogenesis stimulator; angiogenic index;
ion; cancer; coronary artery disease; myocardial ischemia;
eriosclerosis; forensic medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                             Kovacs
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                          296pp;
                                                                                                                                                                                                                                                                                                                                                             Fan W,
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Pred. No. 1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of determining the angiogenic index of a tissue or cell sample comprising assessing, in a sample, the expression levels of one or more differentially-expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative of the angiogenic index. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating cancer, coronary artery disease, myocardial ischemia or coronary artery disease, myocardial ischemia or coronary artery disease, myocardial ischemia of coronary artery disease, myocard
                                                                                                                                                                        The invention relates to a lubricating polypeptide and at least one O linked oligosaccharide. The composition and methods are useful for lubricating joints or other tissues to prevent or treat camptodactylarthropathy pericarditis (CAP) or osteoarthritis in mammals. The pressequence represents the amino acid sequence of the human megakaryocytometric sequence of the sequence of the human megakaryocytometric sequence represents the amino acid sequence of the human megakaryocytometric sequence represents the amino acid sequence of the human megakaryocytometric sequence represents the amino acid sequence of the human megakaryocytometric sequence represents the amino acid sequence of the human megakaryocytometric sequence represents the sequence represents the sequence of the human megakaryocytometric sequence represents the sequence of the human megakaryocytometric sequence represents the sequence 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New tribonectin polypeptides and polynucleotides for lubricating joints or other tissues to prevent or treat Camptodactyl-arthropathy-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADM98015.
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24-APR-2000; 2000US-00556246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lubricating polypeptide; O-linked oligosaccharide; joint lubrication;
CAP; camptodactyl-arthropathy pericarditis; osteoarthritis; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human megakaryocyte stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-2004
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                                                                                                              sequence represents the amino acid sequence of stimulating factor (\mathsf{MSF}).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pericarditis syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-373948/35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADM98014 standard; protein; 1404 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JAYG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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           1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Mismatches
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1.5e+03;
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                                                                                                                                                                              als. The present megakaryocyte
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Query Match
Best Local Similarity
Matches 6; Conserv

Conservative

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Score 33; DB Pred. No. 1.5e 0; Mismatches

DB 8;

Length 1404;

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                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                       lymphangiogenesis or angiogenesis in a mammal, and for modulating the growth of mammalian endothelial cells, mammalian endothelial precursor cells or hematopoietic progenitor cells. The polypeptide may also be used for promoting recruitment, proliferation, differentiation, migration or survival of neuronal cells or neuronal precursor cells, and for treating neurodegenerative discorder, e.g. Alzheimer's diseases, Parkinson's disease, Huntington's disease, motor neuron disease, Parkinson's clerosis (ALS), dementia, or cerebral palsy. The present sequence represents a human heparin binding protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heparin binding protein; Neuroprotective; Nootropic; Antiparkinsonian; Anticonvulsant; VEGF-3 receptor; Anglogenesis stimulator; Gene Therapy; vascular endothelial growth factor reform 3; VEGF-3; angiogenesis disorder; neurodegenerative disorder; Alzheimers disease; parkinsons disease; motor neurone disease; dementia; paralysis; VEGF-C; neurological disease; Huntingtons chorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to heparin-binding vascular endothelial growth factor receptor 3 (VEGFR-3) proteins and encoding polynucleotides. The heparin binding VEGFR-3 proteins are used for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New heparin-binding Vascular Endothelial Growth Factor Receptor 3 ligands comprising prepro-VEGF-C, prepro-VEGF-D sequences or fragments, for treating neurodegenerative disorder, e.g. Alzheimer's, Parkinson's, or Huntington's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LICN )
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12-JUN-2003; 2003US-0478390P.
23-SEP-2003; 2003US-00669176.
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                                                                                                                                                                                                                                                     Sequence 1404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUN-2004; 2004WO-US019122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vascular endothelial growth factor receptor 3; neurological disease
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                                                                                                                              Conservative
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                                                                                                                                                        86.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219pp;
                                                                                                                              <u>.</u>
                                                                                                                                                        Score 33; DB 9;
Pred. No. 1.5e+03;
                                                                                                                              Mismatches
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RESULT 29
ADV15658
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ADV15
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RESULT 30
AED66477
ID AED666XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid encoding a PN polypeptide. The polypeptide, agonist or an antagonist, antibody composition, and method are useful for diagnosing and treating related disorder, e.g. systemic lupus erythematosus, rheumatoid arthitis. The present sequence represents a DNA encoding a PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic; Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic; Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
                                                                                                      Wound healing agent vulnerary; injury; lubricin.
                                                                                                                                                                                                          Human lubricin protein sequence.
                                                                                                                                                                                                                                                              29-DEC-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1464; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WMLSPFS 1177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                  agent; tissue regeneration; antisense therapy;
jury; fractures; osteopathic; synovitis; inflam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.8%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33;
Pred. No.
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RESULT 31
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Best Local S
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                                                                       23-JUL-2004; 2004US-0590766P
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                    arthropathy; musculoskeletal disease; pharmaceutical; therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Megakaryocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2006
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   (MUCO-)
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MUCOSAL
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THERAPEUTICS LLC
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85.7%;
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Pred. No. 1.5e+03;
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                                                                                                                                                                                                                                          New isolated tribonectin comprising a boundary-lubricating amount polypeptide, and an O-linked oligosaccharide group, for use in trearthritic diseases, and to coat artificial limbs and joints.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprises nyaturonic acid (1-5 mg/ml) and tribonectin (10-250 mu g/ml) and tribonectin (10-250 mu g/ml) acid described is the use of tribonectin in the preparation of a medicament for the lubrication and chondroprotection of a mammalian tribonection of a mammalian acid the tribonectic of a mammalian tribonectic tribonectic or an acid tribonectic or an acid tribonectic or an acid tribonectic or acid trib
                                                                                                                                                                Claim 1; SEQ ID NO 1; 34pp; English.
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N-PSDB; AEF89840.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-APR-2000; 2000US-00556246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tribonectin; arthritis; antiarthritic; megakaryocyte stimulating factor; MSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human megakaryocyte stimulating factor (MSF) - SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-APR-2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEF89839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEF89839 standard; protein; 1404 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a viscosupplementation composition (7 comprises hyaluronic acid (1-5 mg/ml) and tribonectin (10-250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Visco-supplementation chondroprotection of r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US7001881-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RHOD-) RHODE ISLAND HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1171 WMLSPFS 1177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00298970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n composition, useful for the lubrication mammalian joint, comprising hyaluronic ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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Pred. No.
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1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoarthritis; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1404;
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The invention comprises a tribonectin protein (a boundary lubricating polypeptide), the tribonectin protein of the invention comprises the human megakaryocyte stimulating factor (MSF) protein. The tribonectin

85.7%;

Pred. No. 1.5e+03;

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RESULT 33
AAU32262
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                             polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation, to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. CC shimulation, as anti-inflammatory agents; and in treatment of leukaemias. CC secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein of the invention is useful for treating arthritic disease and osteoarthritic disease, and for coating artificial limbs and joints prior to implantation. The present amino acid sequence represents the human MSF protein of the invention.
                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for
                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopolesis; nerve tissue regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human secreted protein #2753.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU32262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU32262 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1404 AA;
Sequence 1415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-611725/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                  20; Page 573; 765pp; English
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Pred. No. 1.5e
0; Mismatches
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1.5e+03;
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Query Match

86.8%;

Score 33;

DB 4.

Length 1415;

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Matches 6; Conserv
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22-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
30-AUG-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
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14-AUG-2000;
18-AUG-2000;
                                                                                                                                              14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                            14-AUG-2000;
14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune/haematopoietic antigen SEQ ID NO:10323.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1182 WMLSPFS 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune; haematopoietic; immune/haematopoietic antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; vaccine; metastasis
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        2000US-0217496P
2000US-0220964P
2000US-0220964P
2000US-0224519P
2000US-0225514P
2000US-0225214P
2000US-0225266P
2000US-0225266P
2000US-0225267P
2000US-0225276P
2000US-0225757P
2000US-0225757P
2000US-0225759P
2000US-0225759P
2000US-0225759P
2000US-0226279P
2000US-0228924P
2000US-0229344P
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2000US-0229345P
2000US-0229345P
2000US-0229345P
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2000US-0216880P.
2000US-0217487P.
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                                                                                                                                                                                                                                                                                                                   2000US-0209467P.
2000US-0214886P.
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2000US-0231242P.
2000US-0231243P.
2000US-02312413P.
2000US-0231413P.
2000US-0231414P.
2000US-0232081P.
2000US-0232081P.
2000US-0232398P.
2000US-0232398P.
2000US-0232399P.
2000US-0232399P.
2000US-0232399P.
2000US-0232401P.
2000US-0232401P.
2000US-0232401P.

2000US-0233064P. 2000US-0233065P. 2000US-0234223P. 2000US-0234274P. 2000US-023497P.

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RESULT 35
ABP04103
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AC ABP04
AC ABP04
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XX
DT 25-JU
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                                                                                                                                                                                                                                                                                                                                                         CC AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CI treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CI that affect the activity of (I) by expressing inactive proteins or to Supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting the CC nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent.

CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK64902 to AAK87694 represent necessary immune/haematopoietic antigen genomic CC represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                         Matches
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17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
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Human; open reading frame; ORFX; gene therapy; cancer; hyperproliferative disorder; psoriasis; benign tumour;
                                           Human ORFX protein sequence SEQ ID NO:8188.
                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding
                                                                           25-JUN-2002
                                                                                                                                    ABP04103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                   standard; protein;
                                                                                                                                                                                                                                                                                                                                   31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preventing,
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                                                                         entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben
                                                                                                                                                                                                                                                                      ; Score 32; DB; Pred. No. 39; 0; Mismatches
                                                                                                                                    81
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                                                                                                                                                                                                                                                                                                    Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen polypeptides, cancers and metastasis.
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cirrhosis;
haemorrhage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, costeoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, disorders, systemic through the process of the ster storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form all of the printed specification, but was obtained in electronic compared all of the printed specification, but was obtained in electronic compared to the printed specification but was obtained in electronic compared to the printed specification but was obtained in electronic compared to the printed specification but was obtained in electronic compared to the printed specification but was obtained in electronic compared to the printed specification but was obtained in electronic compared to the printed specification but was obtained in electronic compared to the printed specification but was obtained in electronic compared to the printed specification but was obtained in electronic compared to the printed specification but was obtained to the compared to the printed specification but was obtained to the compared to the printed specification to the printed specification to the printed specification to the printed specification to the printed specific
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes substantially purified human proteins (referred to as open reading frame, OREX, where X is 1-11491 (see Tabin the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 8188; 1037pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000;
29-AUG-2000;
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                            ADC95262;
                                                                             ADC95262 standard; protein; 103 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-106308/14.
DB; ABN19855.
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                                                                                                                                                                                                                                                                                                                      Similarity 5; Conserv
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2000US-0228716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                         Score 32; DB
Pred. No. 1.1e
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                      1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                             DB 5;
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                                                                                                                                                     RESULT 37
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                                                                                                                                                                                                                                                                                                                                                                     recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions resulting from E. faecium bacterial infection (e.g. urinary tract infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccine; urinary tract infection; bacteraemia; endocarditis; wound; abdominal-pelvic infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faecium encoding an Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid derived from Enterococcus faecium encoding Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-1997;
14-MAY-1998;
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                                                             18-DEC-2001
                                                                                                                      AAU25590 standard; protein;
                                                                                                                                                                                                                                                                                                                           Sequence 103
                                                                                                                                                                                                                                                                                                                                                        treating Enterococcus faecium infections. one if the disclosed E. faecium proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 4889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doucette-Stamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENO-) GENOME
                                                                                                                                                                                                                                                                               Local
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WMISAF
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                                                             (first
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98US-0085598P
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                                                             entry)
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                                                                                                                                                                                                                                                                             84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243pp; English
                                                                                                                                                                                                                                                             Score 32; DB Pred. No. 1.4e
1; Mismatches
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1.4e+02;
0;
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Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia;

Human G Protein-Coupled Receptor (GPCR) polypeptide #37

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Matches
                                                                                                                            Query Match
Best Local Similarity
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23-FEB-2000
23-FEB-2000
23-FEB-2000
02-FEB-2000
02-MAR-2000
03-MAR-2000
03-MAR-2000
13-MAR-2000
13-APR-2000
                                                                                                                                                                                                                                                                                             (GPCR) polypeptides of the invention. The proteins and their associated DNA sequences can be used to identify compounds which bind to GPCR polypeptides and in screening for compounds that modulate GPCR activity. By screening a human subject for the presence of mutations in GPCR DNA, GPCR-related disorder or a genetic predisposition can be diagnosed. The sequences can also be used for treatment and prevention of mental disorders such as schizophrenia, attention deficit disorder, anxiety, depression, dementia and bipolar disorder, neurological disorders such as Huntington's disease, Parkinson's disease and Tourette's syndrome, metabolic disorders such as obesity, anorexia and type 2 diabetes, cardiowascular disorders such as thrombosts, myocardial infarction, cardiowascular disorders such as thrombosts, myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid encoding a new G-protein coupled receptor polypeptide for detecting receptor modulators that can treat mental disorders, such as schizophrenia, anxiety, depression, or obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences AAU25554-AAU25616 represent human G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV,
                                                                                                                                                                                                       Sequence 211
                                                                                                                                                                                                                                                                                   cardiomyopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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WLLAAFS 134
                                                   WMLSAFS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wood LS,
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2000US-0184397P.
2000US-0186457P.
2000US-0186810P.
2000US-018680P.
2000US-018880P.
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2000US-02137369P.
2000US-021837P.
2000US-021837P.
2000US-021837P.
                                                                                                   Conservative
                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                   and atherosclerosis, viral infections caused by HIV and
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                                                                                                                            84.2%;
71.4%;
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                                                                                                   2.
                                                                                                                            Score 32; DB 4;
Pred. No. 3.1e+02
                                                                                                   Mismatches
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                                                                                                 Gaps
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RESULT 38 ADR09699

RESULT 39 ABO73613 ID ABO73

AB073613

standard; protein; 262

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                                                                                                                                                                             This invention relates to novel, isolated full length human cDNA CC molecules and the encoded proteins thereof. Specifically, it refers to CC cDNA clones obtained by an oligo-capping method, where none of these CC clones are identical to any known human mRNAs. The present invention CC describes an immunoassay to identify agonists and antagonists, as well as CC antibodies, antisense molecules and siRNAs that can all be used to bind CC and modulate expression of the cDNA molecules. As such, these CC molecules are useful for diagnostic markers or therapeutic targets for CC the various diseases or morbid states. In particular, they are useful in CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's CC disease, Parkinson's disease, dementia, short memory and various cancers, CC as well as for maintaining equilibrium of sense or motor function, and CC as well as for maintaining equilibrium of sense or motor function, and CC cytostatic and tranquiliser activities. This particular accordingly, CC they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, CC cytostatic and tranquiliser activities. This sequence is not given in the sequence of the invention. NOTE: This ceftical be obtained on CD-ROM from the European Patent Office, Vienna Sub-
                                                                 Matches
                                                                               Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; sense or motor function; emotional reaction; fear response; panic; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
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Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-FEB-2003; 2003JP-00102207.
09-MAY-2003; 2003JP-00131452.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADR07743.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tranquiliser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR09699 standard; protein; 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2004-583265/57.
 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein useful for treating neurological disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligo-capping method; diagnostic marker; gene the orosis; neurological disease; Alzheimer's disease;
                               1 WMLSAFS 7
                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
WKLSAFS 193
                                                                                                                                  243 AA;
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A, Ishii S,
                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3205;
                                                                                 84.2%;
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                                                                 Score 32; DB Pred. No. 3.6e 0; Mismatches
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                                                                                   .6e+02
                                                                                                 Length 243;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq 3205
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RESULT 40
AAG81234
ID AAG81
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AC AAG81
XX
DT 04-SE
XX
DE Mycok
XX
KW Drug
XX
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                      including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa poppides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment c pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 22359; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-1998;
27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa polypeptide #5788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUL-2004 (first entry)
             Drug target; growth; organism viability; characterisation
                                               Mycobacterium tuberculosis potential drug target protein SEQ
                                                                                                                                                                                                                                                                                                                                                          Sequence 262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-1999;
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                                                                                04-SEP-2001
                                                                                                                                             AAG81234 standard; protein; 280 AA
                                                                                                                                                                                                                                                                                                                                                                                       seqdata.uspto.gov/sequence.html
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                                                                                                                                                                                                                            234 WMLSAIS 240
                                                                                                                                                                                                                                                          1 WMLSAFS 7
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                                                                                                                                                                                                                                                                                            Conservative
                                                                            (first entry)
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98US-0094190P.
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                                                                                                                                                                                                                                                                                                          84.2%;
85.7%;
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Pred. No. 3.9e+02;
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RESULT 41
AAM51647
ID AAM51
XX AAM51
XX AAM51
XX AAM51
XX Humar
XX Humar
XX Humar
XX Homo
DE Homo
XX Homo
XX Homo
XX Homo
PN WO200
XX HOMO
PN W200
XX HOMO
PF 24-AH
PR 24-AH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polymucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAGB1096 - AAGB1241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1999; 99US-0165086P
12-NOV-1999; 99US-0165124P
01-FEB-2000; 2000US-0179531P
24-APR-2000; 2000US-0199149P.
04-AUG-2000; 2000US-00633146.
                                            24-APR-2001; 2001WO-US013097
                                                                         01-NOV-2001
                                                                                                                                    Homo sapiens
                                                                                                                                                                                                              Human GPCR polypeptide
                                                                                                                                                                                                                                              20-FEB-2002
                                                                                                                                                                                                                                                                           AAM51647;
                                                                                                                                                                                                                                                                                                       AAM51647 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a method for identifying a nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 190; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAH52085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eisenberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-2000; 2000WO-US031152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                         WO200181409-A2
                                                                                                                                                                                 Human; G-protein coupled receptor; GPCR; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                               proto-oncogene receptor; human protease; disease
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                                                                                                                                                                                                                                                                                                                                                                                  262
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5; Conserv
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                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.2%;
71.4%;
                                                                                                                                                                                                                                                                                                         289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 4;
Pred. No. 4.2e+02;
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RESULT 42
AD029555
ID AD0295
XX AD0295
AC AD029
XX AD09-S
YX AD09-S
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Matches
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                                                                                                                                                                                                                                                                                                                                                         G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; nutritive disorder; cancer; joint disorder; metabolic disorder; nutritive disorder; cancer; kidney disorder; there disorder; lung disorder; breast disorder; kidney disorder; tutrus disorder; prostate disorder; testis disorder; skin disorder; stomach disorder; pancreas disorder; spleen disorder; skin disorder; stomach disorder; pancreas disorder; spleen disorder; skin disorder; thyroid disorder; antiparkinsonian; antimanic; cytostatic; antiflammatory; vasotropic; antidarrhostc; antidiabetic; virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic; dermatological; antiparkinsonia, antiseborrhoeic; imminosiania, antiseborrhoeic; antidiabetic; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated human G protein-coupled receptor (GPCR) polypeptide that is related to the MAS proto-oncogene receptor subfamily. The polypeptide comprises a fully defined sequence of 289 amino acids as given in the specification, or its fragment comprising 10 contiguous amino acids, or an amino acid sequence of an allelic variant or orthologue of the amino acid sequence given in the sequence. The polypeptide is useful for identifying a modulator of a GPCR polypeptide or an an agent that binds to it. The polypeptide is also useful for treating a disease or condition mediated by human proteases. The present sequence is the polypeptide of the invention
                           09-SEP-2002; 2002US-0409303P
09-APR-2003; 2003US-0461329P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                     09-SEP-2003; 2003WO-US028226
                                                                                                                                                            13-MAY-2004.
                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                               murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse GPCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO29555 standard; protein; 289 AA.
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                                                                                                                                                                                                                                                                                                                                        immunosuppressive; nephrotropic; gene therapy; GPCR modulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE )
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                                                                                                                                                                                                                                                                                                                  receptor.
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71.4%;
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Pred. No. 4.3e+02;
2; Mismatches 0
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Human GPCR

8N

(MRGG), SEQ ID NO:656.

(first entry)

G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; immune disorder; bone disorder joint disorder; metabolic disorder; nutritive disorder; cancer;

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94

WLLAAFS 100

1 WMLSAFS

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RESULT 43

ADO29554 standard; protein;

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of the invention; methods of treating, preventing or diagnosing diseases compounds useful in the treatment of GPCR-related diseases; a transgenic compounds useful in the treatment of GPCR-related diseases; a transgenic compounds useful in the treatment of GPCR-related diseases; a transgenic compounds useful in the treatment of GPCR-related diseases; a transgenic compounds of the invention; a mouse comprising a computation in a GPCR gene of the invention; a mouse comprising a computation in a different GPCR gene of the invention; and kits comprising composes which hybridise to GPCR polymucleotides of the invention. The comprising a GPCR mucleic acid. The GPCR polymeptides and vectors comprising a GPCR mucleic acid. The GPCR polymeptides and vectors comprising a GPCR mucleic acid. The GPCR polymeptides and vectors comprising a GPCR mucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, comprising a GPCR mucleic acids and proteins may compared to the adrenal gland; disorders of the colon or intestine composession, diabetic neuropathy, Parkinson's disease or schizophrenia); composersion, diabetic neuropathy, Parkinson's disease or schizophrenia); composers of the adrenal gland; disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders (e.g., angina, cardiac arrhythmia or composers (e.g., angina, cardiac arrhythmia or composers); bone and joint disorders (e.g., astoimmune disorders (e.g., atoimmune disorders (e.g., atoimmune disorders (e.g., atoimmune disorders (e.g., acident printiple); and disorders of the kidney, liver, lung, breast, ovary, composition, parking, preast, ovary, and the printed specification; those sequence represents a GPCR of the colon or the printed specification; those sequences not shown were obtained in celectronic format directly from WIPO at this patent did not form part of the printed specification; those sequences not shown were obtained in c
    Matches
                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids
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5; Conserv
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                                                                                            289 AA;
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  Conservative
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                        84.2%;
71.4%;
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Pavlova MN, Vassilatis D,
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  Score 32; DB Pred. No. 4.3e 2; Mismatches
                          4.3e+02;
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mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypuptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurolicital discourse for the comprision of the diagnosis, treatment or prevention of a wide variety of diseases including neurolicital discourse for the comprision of a wide variety of diseases.
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                                        uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus thyroid (e.g., cancers). The present sequence represents a GPCR of invention. Note: The full sequence data for this patent did not for of the printed specification; those sequences not shown were obtain electronic format directly from WIPO at
                                                                                                                                                                                                                                                                             AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatold arthritis, gout or osteoaporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., angina);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-SEP-2002; 2002US-0409303P
09-APR-2003; 2003US-0461329P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GPCRs) and nucleic acids encoding them. The invention also relate sequences at least 90% identical to the GPCR proteins and nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compounds useful in the treatment of GPCR-related diseases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human and mouse G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or leukaemia);
.int/pub/published_pct_sequences
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Mcilwain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 656; 542pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune disorders (e.g., autoimmune disorders or
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Pavlova MN,
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lova MN, Vassilatis D,
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23-FEB-2000;
23-FEB-2000;
23-FEB-2000;
23-FEB-2000;
02-MAR-2000;
03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attention deficit disorder; anxiety; depression; bipolar disorder; neurological disorder; Huntington's disease; dementia; obesity; ance metabolic disorder; Parkinson's disease; Tourette's syndrome; throm type 2 diabetes; cardiovascular disorder; myocardial infarction; cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV; antideavecant
                   Sequences AAU2554-AAU25616 represent human G-protein coupled receptor (GPCR) polypeptides of the invention. The proteins and their associated DNA sequences can be used to identify compounds which bind to GPCR polypeptides and in screening for compounds that modulate GPCR activity. By screening a human subject for the presence of mutations in GPCR DNA, a gPCR-related disorder or a genetic predisposition can be diagnosed. The sequences can also be used for treatment and prevention of mental disorders such as schizophrenia, attention deficit disorder, anxiety, depression, dementia and bipolar disorder, neurological disorders such as
                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid encoding a new G-protein coupled receptor polypeptide for detecting receptor modulators that can treat mental disorders, such as schizophrenia, anxiety, depression, or obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-2000;
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13-MAR-2000;
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2000US-0184397P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anorexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 45
ABB06257
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Matches
                             Matches
                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                  The present sequence represents a human guanine nucleotide binding protein (G protein)-coupled receptor protein designated TGR15. TGR15 has nootropic, antinflammatory, vasotropic, immunomodulator and cytostatic activities. The TGR15 polynucleotide and protein can be used in gene therapy and protein therapy. G-protein coupled receptor proteins are cell membrane proteins which mediate the cellular response to a large variety of signalling molecules. The TGR15 polynucleotide and protein can be used in the diagnosis, treatment and prevention of diseases including neurological, inflammatory, circulatory, degenerative, immune system and discretive diseases.
                                                                                                                                                                                                                                                                                  G-protein coupled receptor protein TGR15 of human origin and DNA encoding it for diagnosis and treatment of cancer and circulatory and other diseases associated with its expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metabolic disorders such as obesity, anorexia and type 2 diabetes, cardiovascular disorders such as thrombosis, myocardial infarction, cardiomyopathy and atherosclerosis, viral infections caused by HIV
                                                                                                                                                                                                                                                        Claim 1; Fig 2; 103pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                               Moriya
                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUL-2000; 2000JP-00211987
26-DEC-2000; 2000JP-00395566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-2001; 2001WO-JP005876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                               Sequence 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200204639-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   digestive disease; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurological; inflammatory; circulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vasotropic; immunomodulator; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human G protein-coupled receptor TGR15 protein SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB06257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB06257 standard; protein; 323
                                                                                                                                                                                                                                                                                                                                                                                                          (TAKE ) TAKEDA CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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DB; ABL40211.
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                             5
                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein-coupled receptor; TGR15; nootropic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WLLAAFS 134
    WMLSAFS
                                                                                                           diseases
                                                                                                                                                                                                                                                                                                                                                                              Ito
                           Conservative
                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                           and cancer
                                                                                                                                                                                                                                                                                                                                                                               Shintani Y,
                                                                                                                                                                                                                                                                                                                                                                                                          IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                       84.2%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB Pred. No. 4.9e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2:
                             2
                                        Score 32; DB 5;
Pred. No. 4.9e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                               Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; I
4.9e+02;
                                                                                                                                                                                                                                                                                                                                                                               z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy; protein therapy;
degenerative; immune system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                   Length 323;
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                          Gaps
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RESULT 46
ABJ10905
ID ABJ1
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                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAR-2001; 2001US-0273946P.
16-MAR-2001; 2001US-0276873P.
30-MAR-2001; 2001US-0280531P.
30-MAR-2001; 2001US-0280596P.
16-NOV-2001; 2001US-033426P.
28-NOV-2001; 2001US-0334229P.
11-JAN-2002; 2002US-0347703P.
                                                                                                                                                                      The invention comprises the amino acid and coding sequences of human secreted proteins (SECP). The human SECP DNA and protein sequences of tinvention are useful for the treatment and prevention of cell proliferative disorders (e.g. actinic keratosis, arteriosclerosis, bursitis, hepatitis or cancer); autoimmune/inflammatory disorders (e.g. ALDS, asthma, anaemia, allergies or atopic dermatitis); cardiovascular disorders (e.g. congestive heart failure, ischaemic heart disease, myocardial infarction, hypertensive heart disease, or vascular tumours) neurological disorders (e.g. epilepsy, stroke, cerebral neoplasme, or Alzheimer's disease); and developmental disorders (e.g. renal tubular acidosis, Cushing's syndrome, Duchenne and Becker muscular dystrophy, chypothyroidism). The present amino acid sequence represents a human secreted protein (SECP) of the invention
                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human secreted proteins and nucleic acids useful in diagnosing, treating and preventing cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, and developmental disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABT11179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAR-2002; 2002WO-US007719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epilepsy; cerebral neoplasm; Alzheimer's disease; developmental Cushing's syndrome; muscular dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell proliferative disorder; autoimmune disorder; inflammatory disorder; AIDS; asthma; anaemia; allergy; atopic dermatitis; myocardial infarction; cardiovascular disorder; vascular tumour; neurological disorder; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein (SECP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-713444/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gururajan R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thangavelu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABJ10905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n; gene therapy; secreted protein; sproliferative disorder; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|:|||
128 WLLAAFS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang J
elu K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INCYTE GENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; protein; 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                       A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J, Elliott VS, Duggan BM,
Gietzen KJ, Forsythe IJ,
Lal PG, Baughn MR, Xu Y,
Kallick DA, Walia NK, Mask
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126-127; 162pp; English.
                               84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secreted protein; SECP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC
Score 32; DB 5;
Pred. No. 5.7e+02;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Honchell CD, Lee S;
Lu DAM, Griffin JA;
Tang YT, Azimzai Y;
on PM, Tran UK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatitis;
                                                           Length 371;
                                                                                                                                                                                                                                                                                                                                          tumours);
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Matches

6;

Conservative

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Gaps

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RESULT 47
ABO60886
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XX ABO60
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ADF70484
ID ADF7
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AC ADF7
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AC ADF7
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AC DT 12---
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UT 12---
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UT 12---
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CFP
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CGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                RESULT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                            ligand; orphan receptor protein; fusion protein; fluorescent protein; cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP; GFPuv; Enhanced GFP; EGFP; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a new isolated nucleic acid encoding a Klebsiel pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 7403; 932pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preparing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Breton GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6610836-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klebsiella
                                                                                                                                   Orphan receptor
                                                                                                                                                                                        12-FEB-2004
                                                                                                                                                                                                                                           ADF70484;
                                                                                                                                                                                                                                                                                           ADF70484 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENO-) GENOME THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003-895346/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                 391 WSLSAFS 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WMLSAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WKLSAFS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WMLSAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pneumoniae polypeptide seqid 7403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                      (first
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                                                                                                                                   ligand-related human
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                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.2%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB
Pred. No. 6.7e
0; Mismatches
                                                                                                                                                                                                                                                                                             561 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
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                                                                                                                                   protein SeqID107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7; Le...
. 6.7e+02;
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RESULT 49
ADU02401
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KW Cytos
KW proli
KW metak
KW proli
KW metak
KW ulcei
XX Homo

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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a novel method of identifying ligands to an orphan receptor protein which comprises transforming cells with DNA encoding a fusion protein of the orphan receptor with a fluorescent protein, so that the fusion protein is expressed in the cells (or cell membranes isolated from them) and contacting the cells with the potential ligand to be tested. A suitable fluorescent protein for incorporation in the fusion protein is green fluorescent protein (GFP), for example GFP-1, wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the identification of ligands binding to an orphan receptor protein.
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23-JUL-2002; 2002JP-00213949
11-OCT-2002; 2002JP-00298237
  18-APR-2003; 2003US-0463708P
18-APR-2003; 2003US-0463732P
02-MAY-2003; 2003US-0467199P
02-MAY-2003; 2003US-0467230P
                                                                                                                                                                                                                                                                                                                                                        cytostatic; antipsoriatic; antiinflammatory; gene therapy; Nanodisc; proliferative disorder; inflammatory disorder; immune disorder; metabolic disorder; bone disorder; CNS disorder; cancer; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transformation of cells with a fusion protein protein with a fluorescent protein useful for
                                                                                                                                                                                 04-NOV-2004
                                                                                                                                                                                                                                                                                                                                   ulcerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human polypeptide seqid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADU02401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADU02401 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the orphan receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2003; 2003WO-JP001901
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                                                                                                                              19-APR-2004; 2004WO-US012047
                                                                                                                                                                                                                                  WO2004093804-A2
                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003-697654/66.
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5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujii R,
                                                                                                                                                                                                                                                                                                                                   colitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IND LTD
                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32;
Pred. No.
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J.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of an orphan receptor identification of ligands
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host cell transformed, transfected, transduced or infected with the conclusive acid molecule; a nucleic acid composition comprising a carrier or ca buffer and one or more compositions comprising the nucleic acid composition for nucleic acid compositions one prising the polypeptide; and a carrier or buffer; a cell comprising the polypeptide; a polypeptide composition comprising the polypeptide; and a carrier or buffer; a cell culture medium comprising the polypeptide and a carrier or buffer; a cell culture medium comprising the polypeptide or transfected cells transfected with the polynucleotide; making a transformed, transfected, culture medium comprising the propertide or transfected Nanodiscs simultaneously or infected host cell; synthesising Anodiscs simultaneously cand for synthesising a series of simultaneously-synthesised Nanodiscs sequentially utilising a dynamic system; preparing a hydrophobic protein corystal structure; immunising a non-human animal; corecening for modulators of hydrophobic protein activity; a diagnostic kit determining the presence of the nucleic acid molecule or its complement; determining the presence of an antibody to the polypeptide in a sample; an antibody specifically recognising, binding to or modulating cold acid molecule or its biological activity of at least one polypeptide encoded by a nucleic acid molecule or its biologically collaboration or its biological activity of at least one polypeptide encoded by a nucleic acid molecule or its biologically collaboration or its biologically collaboration or its biologically collaboration of the polypeptide in a collaboration or its biological activity of at least one polypeptide in a collaboration of the polypeptide in the polypeptide
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14-JUL-2003;
08-AUG-2003;
                                                                                                                                                                                                                                      antibody; diagnosing a disease, disorder, syndrome, or condition comprising cancer, or proliferative, inflammatory, immune, metabolic, bone, CNS, genetic, bacterial and viral diseases, disorders, syndromes or conditions in a patient; a modulator composition comprising a modulator and a carrier; gene therapy; prophylactic or therapeutic treatment of a subject; an isolated modified cell comprising at least one first heterologous nucleic acid molecule, where the first heterologous nucleic acid molecule, where the first heterologous nucleic acid molecule, where the first polypeptide; a non-human animal deficient in the polypeptide or that the polypeptide or the first polypeptide or the first polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid molecule or its biologically active fragment; an antibody composition comprising the antibody and a carrier; a bacteriophage, where the antibody is displayed on the bacteriophage; a bacterial cell comprising the bacteriophage; a non-human animal injected with the antibody composition; a host cell that secretes the antibody; making an antibody composition; a host cell that secretes the antibody; making an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an animal injected with the nucleic acid morecule, a least molecule comprising a second polynucleotide sequence that is at least about 70, 80, 90 or 95% homologous to the first nucleic acid molecule or that hybridises to the first polynucleotide sequence under high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a new first nucleic acid molecule comprising a polynucleotide sequence given in the specification. Also described are: an animal injected with the nucleic acid molecule; a second nucleic acid molecule comprising a second polynucleotide sequence that is at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stringency conditions; a vector comprising the nucleic acid molecule and a promoter that drives the expression of the nucleic acid molecule; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New first nucleic acid molecule comprising a polynucleotide sequence given in the specification, useful in preparing a composition for diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-AUG-2003;
08-SEP-2003;
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08-JUL-2003;
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19-MAY-2003;
                                                                                                               diagnosing or
                                                                                                                                                                                        non-human
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                                                                           over-expresses the polypeptide; isolated tissues derived from the human animal; and one or more cells derived from the non-human al. The nucleic acid is useful in preparing a composition for nosing or treating e.g., cancer, psoriasis or ulcerative colitis. In the amino acid sequence of a novel human polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIVE PRIME THERAPEUTICS INC.
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2003US-0471336P.
2003US-0485223P.
2003US-0485224P.
2003US-0486446P.
2003US-0486480P.
2003US-0493573P.
2003US-0493573P.
2003US-0493579P.
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Query Match Best Local Similarity

84.2%; 71.4%;

Score Pred.

32; No.

DB 8; 2e+03;

Length 1180

Sequence 1180 AA;

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ABG21142
IID 21342
IID 21342
IID 21342
AC ABG21
AC ABG21
AC ABG21
XX Human
KW Human
KW Hood
OX Homo
OX Homo
OX Homo
XX Homo
PN W0200
PN W0200
PN W0200
PN W0200
II-OC
FR 30-MA
XX Gree
PR 23-AU
XX WPI;
DR N-PSI
XX WPI;
DR WP
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Best Local Similarity
Matches 5; Conserv
                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                          useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reaction (PCR) primers, oligomers, and for chromosome and gene mappi
and in recombinant production of (II). The polymucleotides are also
in diagnostics as expressed sequence tags for identifying expressed
genes. (I) is useful in gene therapy techniques to restore normal
activity of (II) or to treat disease states involving (II). (II) is
                                                                                                                                                                              and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                         Sequence 1923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reaction (PCR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutatresponsible for genetic disorders or other traits and to asse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT,
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23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US008631.
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RESULT 2  T30536  Typothetical protein 2 - Fugu rubripes (fragment) C:Species: Fugu rubripes C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 # C:Accession: T30536 C:Accession: T30536 R;Riboldi Tunnicliffe, G.R.; Platzer, M.; Nyakatura, submitted to the EMBL Data Library, September 1997	Query Match 89.5%; Score 34; DB 2; Best Local Similarity 85.7%; Pred. No. 32; Matches 6; Conservative 0; Mismatches  Qy 1 WMLSAFS 7               Db 372 WMLSCFS 378	teriol: 17, 1981-1988, 1995 le: Analysis of a novel gene and beta-gala- erence number: A56263; MUID:95238267; PMII sssion: A56263 cus: preliminary scule type: DNA idues: 1-637 -GUT> ss-references: UNIPARC:UPI00000B56E1; GB:U erfamily: beta-galactosidase, BgaH type words: glycosidase; hydrolase	່າ ທ້	468 26 68.4 412 2 G644059 470 26 68.4 417 2 D82172 471 26 68.4 421 2 F83852 472 26 68.4 421 2 F83852 473 26 68.4 422 2 S73369 473 26 68.4 428 2 A55044 474 26 68.4 431 2 T24941 475 26 68.4 433 2 AB3273 477 26 68.4 433 2 AB3273 477 26 68.4 433 2 AB3273 481 26 68.4 433 2 AC0104 481 26 68.4 435 1 S18609 481 26 68.4 430 2 G70693 481 26 68.4 440 2 G70693 484 26 68.4 440 2 G70693 487 26 68.4 444 2 B35794 488 26 68.4 444 2 B35794 489 26 68.4 444 2 B35389 489 26 68.4 447 2 T09414 491 26 68.4 447 2 T09414 491 26 68.4 447 2 T09414 492 26 68.4 450 2 D82328 494 26 68.4 450 2 D82328 495 26 68.4 450 2 D82328 496 26 68.4 450 2 D91280 497 26 68.4 457 2 AD3073 498 26 68.4 460 2 T12694 499 26 68.4 460 2 D92329 499 26 68.4 460 2 D92329 56 68.4 460 2 D92329 56 68.4 460 2 D92329 57 26 68.4 460 2 D92329 58 26 68.4 460 2 D92329
#text_change 09-Jul-2004 	Length 637; 1; Indels 0; Gaps 0;	1.0	Arthrobacter sp. (strain B7) 1995 #text_change 16-Aug-2004 Brenchlev, J.E.	probable serine trasporter perine transporter glutamate dehydrog hypothetical prote beta-4C-darenergic hypothetical prote ABC transporter (pammonium transport probable sugar traregeneration assoc probable sugar transcription fact transcription fact transcription fact transcription fact transcription of antimaturation of antimaturation of antimaturation of antimaturation of antimaturation fact iransporter homolo hypothetical prote pectinesterase hom pmbA protein - Esc permease VCA0904 (maturation of antimaturation of antimaturation of antimaturation of antimaturation prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote thiamin-repressibl probable amino aci

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A;Description: Analysis of the genomic loci of Fugu rubripes homologs of the human dised A;Reference number: Z20848
A;Accession: T30536
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: DNA
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A;Cross-references: UNIPROT:073698; UNIPARC:UPI000001B8E6; EMBL:AF026198; NID:g3098263; C;Genetics:
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A;Experimental source: strain H37Rv
C;Genetics:
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.; A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
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                                                                                                                                                                                                                                                                                  hypothetical protein all0050 [imported] - Nostoc sp. C;Species: Nostoc sp. PCC 7120 C;Species: Nostoc sp. strain PCC 7120 is a synonym of Ar A;Note: Nostoc sp. strain PCC 7120 is a synonym of Ar C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #t
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A;Cross-references: UNIPROT:Q8Z0P0; UNIPARC:UPI00000CDBF9; GB:BA000019; PIDN:BAB77574.1
A;Experimental source: strain PCC 7120
C;Genetics:
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A;Status: preliminary; nucleic acid sequence
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C;Accession: C70696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable transport system permease - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
                                                               A; Molecule type: DNA
A; Residues: 1-345 < KUR>
                                                                                                              A;Status: preliminary
                                                                                                                            A; Accession: AB1813
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Pred. No.
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M.; Yamada,
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; Yasuda, M.; Tabata,
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R;Takami, H; Nakasone, K.; Takaki, L., ...........
R;Takami, H; Nakasone, K.; Takaki, L., .............
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
                                                                                                                                                                                                             R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, F. Virology 189, 304-316, 1992
Virology 189, 304-316, 1992
A;Title: The DNA sequence of equine herpesvirus-1.
A;Reference number: A41831; MUID:92295566; PMID:1318606
A;Contents: annotation; possible protein-coding frames
A;Note: neither amino acid nor nucleotide sequence is gi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.3K capsid protein - equine herpesvirus 1 (strain Ab4p) C;Species: equine herpesvirus 1 C;Species: equine herpesvirus 1 A;Note: host Equus caballus (domestic horse) C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_
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A;Cross-references: UNIPROT:Q9KAL1; UNIPARC:UPI00000C3E6F; GB:AP001515; GB:BA000004; NID
A;Experimental source: strain C-125
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                                                                                                                                     C; Keywords:
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R; Telford, E.A.R.; 1
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A; Accession: E36797
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RESULT 7

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R;Ng, W.V.; Kennedy, S.D.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D. Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: D84181
                                                                                                                                                         A; Reference number: A83650; A; Accession: H83697
                                                                                                                                                                               R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                        hypothetical protein BH0384 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004 C;Accession: H83697
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A;Experimental source: strain LT11
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A; Residues: 1-187 <BOY>
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A; Residues: 1-149 <STO>
A; Cross-references: UNI
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C;Species: Halobacterium sp. NRC-
                     A; Experimental source: C; Genetics:
                                        A;Cross-references: UNIPROT:Q9KFU2; UNIPARC:UPI00000C386B; GB:AP001508; GB:BA000004; NII
A;Experimental source: strain C-125
                                                                                      A; Molecule type: DNA
A; Residues: 1-257 <STO>
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Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession:
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83.3%;
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71.4%;
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Pred. No. 41;
1; Mismatches
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G.; Jabl
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RESULT 12 AD2899

conserved

hypothetical

protein Atu2629

[imported]

Agrobacterium

tumefaciens

(strain

C5

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hypothetical protein AGR_C 4767 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004 C;Accession: 897674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 43/2; 92/1; 186/2
A;Note: AA TM018A10.12
C;Superfamily: Arabidopsis tl
                                                                                                                                                                                                              A;Reference number: A97359; WUID:21608551; PMID:11743194
A;Recession: E97674
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E97674
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                                                                                                  A;Gene: AGR C_4/5/
A;Map position: circular chromosome
                                                                                                                                                                                                                                                               R;Goodner, B.; Hinkle, G.; Gattung, A.; Liu, F.; Wollam, C.; Allinger, Science 294, 2323-2328, 2001
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C;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein A_TM018A10.12 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Feb-1999 #text_
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                                                                                                                                                C; Genetics
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                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-365 < KUR>
                                                                                                                                                                                                       A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, July 1997
A;Description: The sequence of A. thaliana TM018A10
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Matches
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195
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WMLSSF
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                                                          Conservative
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                              S.; Miller, N.; Blanchard, M.; Qurollo, M.; Doughty, D.; Scott, C.; Lappas, C.;
                                                                                                                                                              UNIPARC: UPI00000D28EF; GB: AE007869;
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Markelz,
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ckelz, B.;
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R; Zhang, Y. Z.; Reddy, C.A.; Rasooly, A. Gene 97, 191-198, 1931 and Gene 98, Title: Cloning of several lignin peroxidase (LIP) encoding genes: sequence analysis of A; Reference number: JN0117; MUID:91153647; PMID:1999283
A; Accession: JN0117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diarylpropane peroxidase (EC 1.11.1.14) H10 precursor - basidiomycete (Phanerochaete N;Alternate names: diarylpropane oxygenase; lignin peroxidase GIG5; ligninase C;Species: Phanerochaete chrysosporium C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 12-Jul-2004 C;Accession: JN0117; S13565; E29610; E60995
                                                                                                                                                                                                                                                                                                   Gene 60, 93-102, 1987
A;Title: Analysis of nucleotide sequences of two ligninase A;Reference number: A91587; MUID:88152506; PMID:3440521
                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UPI000004CB03; GB:X55343; EMBIA;Note: the nucleotide sequence was submitted to the EMBL R;de Boer, H.A.; Zhang, Y.Z.; Collins, C.; Reddy, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Gaškell, J.; Dieperink, E.; Cullen, D.
Nucleic Acids Res. 19, 599-603, 1991
A;Title: Genomic organization of lignin peroxidase genes
A;Reference number: S13563; MUID:91187681; PMID:2011531
                                                                                                                                                           A;Cross-references: UNIPARC:UPI000004CB03;
R;Dass, S.B.; Reddy, C.A.
FEMS Microbiol. Lett. 69, 221-224, 1990
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A; Residues: 1-368 < KUR>
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A;Residues: 1-371 <GAS>
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                                            A; Molecule type: protein A; Residues: 28-37 < DAS >
                                                                                           A; Accession: E60995
                                                                                                               A; Reference number: A60995
                                                                                                                                     A; Title: Characterization of
                                                                                                                                                                                                                                                    A; Molecule type: mRNA
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;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                  Accession: B29610
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UNIPARC:UPI00001721E6
De: ATCC 24725
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83.3%;
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Pred. No. 79;
1; Mismatches
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                                                                                                                                                                                                               GB:M18743
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T.; Levy, R.; Li, 
                                                                                                                                                                                                                                                                                                                              CDNAs
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C; Comment: Lignin peroxidases play a key role in the initial depolymerization (C; Genetics: A; Gene; GLG5; LIP6
A; Introns: 21/3; 71/2; 90/1; 161/1; 175/1; 201/2; 243/2; 343/3; 365/2
C; Superfamily: peroxidase
C; Keywords: extracellular protein; glycoprotein; heme; oxidoreductase
C; Keywords: extracellular protein; glycoprotein; heme; oxidoreductase
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-27/Domain: gropeptide #status predicted <SIG>
F;19-37/Domain: propeptide #status predicted <PRO>
F;28-371/Product: lignin peroxidase H10 #status experimental <MAT>
F;283/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lignin peroxidase (EC 1.11.1.-) 2 precursor - basidiomycete N;Alternate names: lignin peroxidase H6; ligninase H6 C;Species: Phanerochaete chrysosporium C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_cha C;Accession: JC1268; JH0491; PS0247; C60995 R;Ritch Jr., T.G.; Gold, M.H.
                                                                                                      C;Keywords: extracellular protein; glycoprotein; heme; oxid F;1-21/Domain: signal sequence #status predicted <SIG> F;22-28/Domain: propeptide #status predicted <PRO> F;29-371/Product: lignin peroxidase #status predicted <
                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Dass, S.B.; Reddy, C.A. FEMS Microbiol. Lett. 69, A;Title: Characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Restdues: 1-371 <RI2>
A;Cross-references: UNIPARC:UPI000012E681; GB:M74229; NID:g169271;
A;Experimental source: strain OGC101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 118, 73-80, 1992
A;Title: Characterization of a highly expressed lignin |
A;Reference number: JC1268; MUID:92380494; PMID:1511887
A;Accession: JC1268
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JC1268
                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPARC:UPI0000175215
A;Experimental source: ATCC 24725
                                                                                                                                                                                                                                                                                                                                                    A; Molecule type:
A; Residues: 29-38
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A; Accession: C60995
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A; Title: Lignin peroxidase
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A; Residues: 1-371 < R
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Best Local
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Local Similarity
mes 6; Conserv
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73-80, 1992
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29-38 <DAS>
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29-48 <RIT1>
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                    81.6%;
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Score 31; DB
Pred. No. 80;
0; Mismatches
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Pred. No.
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lignin peroxidase (EC 1.11.1.-) LIPA precursor - basidiomycete (Phanerochae N,Alternate names: ligninase LIPA C;Species: Phanerochaete chrysosporium C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 12-Jul-2004 C;Accession: S13563
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Nucleic Acids Res. 18, 7173, 1990
A; Title: Nucleotide sequence of a new lignin peroxidase A; Reference number: S13723; MUID:91088334; PMID:2129560
A; Accession: S13723
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C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 12-Jul-2004
C;Accession: S13723
                                                                                                                                                                                                    C;Superfamily: peroxidase
C;Keywords: extracellular protein; glycoprotein; heme; oxidoreductase
C;Keywords: extracellular protein; glycoprotein; heme; oxidoreductase
F;1-28/Domain: signal sequence #status predicted <AGT>
F;29-372/Product: lignin peroxidase LIPA #status predicted <AMT>
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A; Residues: 1-372 <G
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Nucleic Acids Res. 19, 599-603, 1991
A;Title: Genomic organization of lignin peroxidase genes
A;Reference number: S13563; MUID:91187681; PMID:2011531
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A; Residues: 1-372 <NAI>
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Local Similarity 85.7%;
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                                                                                                                               Pred. No.
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lignin peroxidase (EC 1.11.1.-) GLG6 precursor - C;Species: Phanerochaete chrysosporium C;Date: 28-Jun-1991 #sequence_revision 28-Jun-199 C;Accession: A36693
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S01028
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R;Smith, T.L.; Schalch, H.; Gaskell, J.; Covert, J., Curry, J., Nucleic Acids Res. 16, 1219, 1988
A;Title: Nucleotide sequence of a ligninase gene from Phanerochaete A;Reference number: S01028; MUID:88144011; PMID:3344218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N; Alternate names: lignin peroxidase HE
C; Species: Phanerochaete chrysosporium
C; Date: 28-Feb-1990 #sequence_revision
C; Accession: S01028
                                                                                                                                                                                                                           A;Gene: LPOA
A;Introns: 21/1; 72/2;
C;Superfamily: peroxida
C;Keywords: extracellul
                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-372 <SMI>
A; Cross-references: UNIPROT: P06181;
A; Note: the authors translated the C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: extracellular protein; glycoprotein; heme; oxidoredue; f;1-28/Domain: signal sequence #status predicted <SIG>F;2-9-372/Product: lignin peroxidase LIPB #status predicted <MAT>F;285/Binding site: carbohydrate (Asn) (covalent) #status predict
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A;Title: Genomic organization of lignin peroxidase genes of A;Reference number: S13563; MUID:91187681; PMID:2011531
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A; Residues: 1-372 <G/
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N;Alternate names: lignin peroxidase H8; ligninase H8
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85.7%;
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28-Jun-1991

#text\_change

basidiomycete (Phanerochaete

chrysospor

1 WMLSAFS 7

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A;Title: Characterization of a new lignin peroxidase gene (GLG6) from Phanerochaete A;Reference number: A36693; MUID:91097609; PMID:2268360
A;Accession: A36693
A;Status: preliminary; not compared with conceptual translation
A;Roseidance: 1700: UNA
A:Roseidance: 1700: UNA
                                                                                                                                                                                                          Gene 70, 127-137, 1988
A;Title: Molecular analysis of a Phanerochaete chrysosporium A;Reference number: JT0402; MUID:89196904; PMID:3240864
A;Accession: JT0402
                                                                               A;Cross-references: UNIPARC:UPI0000168966; GB:M27884; NID:g169283; PIDN:AAB00798.1; A;Note: the authors translated the codon TGC for residue 41 as Ser, and TCG for resic;Superfamily: peroxidase C;Keywords: extracellular protein; qlycoprotein: heme: oxidoreductace
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C;Superfamily: peroxidase
C;Keywords: extracellular
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A;Residues: 1-372 <WAL>
A;Cross-references: UNIPROT:P06181; UNIPARC:UPI000012E685
C;Genetics:
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A; Residues: 1-372 < AND>
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                 Similarity 85. 6; Conservative
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lignin peroxidase (EC 1.11.1.-) H8 precursor - basidiomycete (Phanerochaete NyAlternate names: ligninase H6 C;Species: Phanerochaete chrysosporium C;Date: 27-Feb-1990 #sequence_revision 31-Dec-1993 #text_change 12-Jul-2004
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A;Gene: liP
C;Function:
A;Description:
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C;Keywords: extracellular protein; glycoprotein; heme;
F;1-28/Domain: signal sequence #status predicted <SIG>
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R;Schneider, H.; Barth, W.; Boehme,
Biol. Chem. Hoppe-Seyler 377, 399-41
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S69246
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A; Residues: 1-372 < AND>
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                                                                                                                                                                                                                                                                                                                      R;Andrawis, A.; Pease, E.A.; Kuan, I.; Holzbaur, I
Biochem. Biophys. Res. Commun. 162, 673-680, 1989
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A;Experimental source: strain BKM-F 1767
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                                                                                                                                                                                                                                                                                                                                                        Species: Phanerochaete chrysosporium; Date: 11-Feb-1993 #sequence_revision; Accession: B43638
                                                                                         Query Match
Best Local
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RESULT 26
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A;Title: Molecular cloning and sequences of lignin peroxidase genes of Phanerochaete chr
A;Reference number: A32322; MUID:89343994; PMID:2761543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: A32322; S66556; D60995
R;Schalch, H.; Gaskell, J.; Smith, T.L.; Cullen,
Mol. Cell. Biol. 9, 2743-2747, 1989
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A;Title: Multiple ligninase-related genes from Phanerochaete chrysosporium
A:Reference number: JS0065; MUID:89211962; PMID:2907500
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A;Experimental source: ATCC 24725
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R;Dass, S.B.; Reddy, C.A.
FEMS Microbiol. Lett. 69, 221-224, 1990
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A;Title: Expression of lignin peroxidase H8 in Escherichia coli: A;Reference number: S66556; MUID:96207556; PMID:8670100
A;Accession: S66556
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A;Note: the authors translated the codon CAG for residue 110 as His, GAC
R;DOyle, W.A.; Smith, A.T.
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A; Residues: 1-372 < SCH>
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A;Residues: 1-372 <BRO>
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A;Accession: JS0065
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R;Brown, A.; Sims, P.F.G.; Raeder, U.; Broda,
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A;Residues: 29-38 <DAS>
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A;Accession: D60995
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                                                                                                                                                                                                                                                                ;Superfamily: peroxidase;Keywords: extracellular protein; glycoprotein; heme; oxidoreductase;1-28/Domain: signal sequence #status predicted <SIG>
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6; Conservation
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C;Accession: B32322
R;Schalch, H; Gaskell, J; Smith, T.L.; Cullen, D.
Mol. Cell. Biol. 9, 2743-2747, 1989
A;Title: Molecular cloning and sequences of lignin peroxidase grantering commences. B32322; MUID:89343994; PMID:2761543
A;Accession: B32322
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
B;Molecule type: DNA
B;Molecule type: DNA
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C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
C;Accession: JH0156
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A;Cross-references: UNIPARC:UPI0000175212
C;Superfamily: peroxidase
C;Keywords: extracellular protein; glycop
                                                                                                                                                                         R;Tien, M.; Tu, C.P.D.

Nature 326, 520-523, 1987

A;Title: Cloning and sequencing of a cDNA for a ligninase from Phanerochaete chrysosporium, a; Title: Cloning and sequencing of a cDNA for a ligninase from Phanerochaete chrysosporium, a; Teference number: A27817; MUID:87173020; PMID:3561490

A;Accession: A27817
                                                                                                                                                                                                                                                                                                                        lignin peroxidase (EC 1.11.1.-) precursor - basidiomycete (Phanerochaete chrysosporium) C;Species: Phanerochaete chrysosporium C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 12-Jul-2004
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A;Title: Characterization of lignin peroxidase-encoding A;Reference number: JH0156; MUID:90323600; PMID:2373364
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C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 12-Jul-2004
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A;Residues: 1-372 <HUO>
A;Cross-references: UNIPROT:P31837; UNIPARC:UPI0000168967; GB:M37701; GB:M22720; NID:g169
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F;1-28/Domain: signal sequence #status predicted <SIG>F;29-373/Product: lignin peroxidase #status predicted
                                                 C;Superfamily: peroxidase
C;Reywords: extracellular protein; glycoprotein; heme; oxidoreductase
                                                                                                  A;Cross-references: UNIPROT:P06181; UNIPARC:UPI0000168965; GB:Y00262; NID:g3149;
                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-373 <TIE>
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    i.; Maentsaelae,

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                                                                                                        PIDN: CA
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RESULT 31
C82120
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T48836
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A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D96955
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A; Residues: 1-416 < KUR>
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transcription regulator AraC/XylS family VC2080 [imported] - Vibrio cholerae C;Species: Vibrio cholerae C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Accession: C82120
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A;Experimental source: cosmid contig 68B2; strain 74
                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Neurospora crassa
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein 68B2.200 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q97LV3; UNIPARC:UPI00000C9E8C; A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Nolling,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sensory transduction histidine kinase (HAMP, HisKA, HATPase C;Species: Clostridium acetobutylicum
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:Accession: D96955
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Best Local
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                                                                                                                                  349
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                                                                                                                                  WMVSAF 354
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85.7%;
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                                                                                                                                                                                                              Score 31; DB Pred. No. 80; 0; Mismatches
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Pred. No.
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Pred. No. 1.1e+02;
1; Mismatches 0;
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A; Introns: 2
C; Superfamil
C; Keywords:
hypothetical protein SPAC17C9.10 - fission yeast (SC;Species: Schizosaccharomyces pombe C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 C;Accession: T11590; T52026 R;Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, April 1996 A;Reference number: Z17295
                                                                                                                                        RESULT 33
T11590
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A;Residues; 1-1121 cHEI>
A;Cross-references: UNIPROT:Q9KQCO; I
A;Cross-references: Enrogroup O1;
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Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data A;Reference number: S41014 A;Accession: S41020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Berks, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell 76, 665-676, 1994
A;Title: Caenorhabditis elegans cell survival gene ced-9
A;Reference number: A53189; MUID:94170367; PMID:7907274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Hengartner, M.O.; Horvitz, H.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytochrome b560 homolog precursor - Caenorhabditis elegans N;Alternate names: hypothetical protein T07C4.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: cyt-1
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A;Residues: 1-182 <BER>
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A; Residues: 1-182 <B
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A;Residues: 1-182 <HEN>
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Pred. No.
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Pred. No.
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09-Jul-2004

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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
probable tetraacyldisaccharide 4'-kinase (EC 2.7.1.130) HI0059 [similarity] C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004 C;Accession: G64141 R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.:
                                                                                                                    RESULT 35
G64141
                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position:
C; Superfamily:
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A;Experimental source: strain ED665h(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-271 < KYU>
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A;Reference number: Z25907
A;Accession: T52026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q10482; UNIPARC:UPI0000136110; EMBL:Z73099; NID:g1314152
A;Experimental source: strain 972h(-)
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A;Molecule type: DNA
A;Residues: 1-305 <STC
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Best Local S
Matches
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;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Genetics:
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71.4%;
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71.4%;
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                                                                                                                                                                                                                                                                                                            Score 30; DB 2;
Pred. No. 1.1e+02;
1; Mismatches 1
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R;Goodner, B; Wollam,
A;Gene: AGR C 1257
A;Map position: ci:
C;Superfamily: Escl
                                                                     A;Molecule type: DNA
A;Residues: 1-348 <KUR>
A;Cross-references: UNIPROT:Q8UHI5; UNIPARC:UPI000012E91B;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                 C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                  A;Title: Genome Sequence of the Plant Pathogen and Biotechnology A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                             Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                       C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                             tetraacyldisaccharide 4'-kinase (lipid a 4'-kinase) [imported] - Agrobacterium
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B.; Hinkle, G.; Gattung, F.; Wollam, C.; Allinger,

S.; Miller, N.; Blanchard, M.; Qurollo, M.; Doughty, D.; Scott, C.; Lappas, C.;

Agent

Agrobacterium

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B.; Goldm Markelz,

Goldman, kelz, B.;

tumefacier

: circular chromosome Escherichia coli pro

probable

tetraacyldisaccharide

4'-kinase

ycaH

GB:AE007869;

PIDN: AAK86507.1;

B97444

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; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                            A;Cross-references: UNIPROT:Q97XT8;C;Genetics:
A;Gene: SSO1619
                                                                                                                                                                                                                                                                                                                                                         R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Char Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 24-May-2001 #sequence_revision
C;Accession: C90322
R;She, Q.; Singh, R.K.; Confalonieri, F
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C;Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycosyltransferase [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus
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A; Accession: C90322
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                                                                                                                                                                                                                                                   A;Residues: 1-341 <KUR>
                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                              A;Status: preliminary
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A;Residues: 1-332 <TIGR>
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                                            1 WMLSAFS
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5; Conserv
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WLLSLFS
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106
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71.4%;
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71.4%;
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Pred. No.
                                                                                                            Score 30; DB 2;
Pred. No. 1.2e+02;
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                                                                                         Mismatches
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1.2e+02;
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C;Species: Vibrio cholerae (strai
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82168
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Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q9KRF2; UNIPARC:UPI00000C3092; GB:AE004247; GB:AE003852; NII
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-374 <HEI>
                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                          A;Reference number: A82035;
A;Accession: E82168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable alpha-1,6-galactosidase VC1690 [imported] - Vibrio cholerae (strain N16961 sero
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C; Superfamily: E
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A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-348 < KUR>
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A;Accession: AC2662
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Best Local Similarity
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Best Local
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                                                                                 Similarity 5; Conserv
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                                        WMLSAF 6
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Bscherichia coli probable tetraacyldisaccharide 4'-kinase
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1; Mismatches
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    Mismatches

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Pred. No. 1.2e+02;
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1.2e+02;
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1.3e+02;
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C;Accession: S65138; G48394
R;Aoki, N.; Kishi, M.; Taniguchi, Y.; Adachi, T.; Nakamura, R.; Matsuda, T.
Biochim. Biophys. Acta 1245, 385-391, 1995
A;Title: Molecular cloning of glycoprotein antigens MGP57/53 recognized by monoclonal A;Reference number: S65138; MUID:96125736; PMID:8541316
A;Accession: S65138
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPARC:UPI0000177800
R;Matcher, I.H.; Banghart, L.R.; Lane, W.S.
Biochem Mol. Biol. Int. 29, 545-554, 193
A;Title: The major fat-globule membrane proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycoprotein antigen MGP57/53, mammary gland - bowine (fragment) N;Alternate names: glycoprotein component 16/major fat-globule m C;Species: Bos printgenius taurus (cattle) C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change
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S65138
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A;Map position: 2
C;Superfamily: tyrosine-specific transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 207-220 <MAT>
A;Cross-references: UNIPARC:UPI000014C31B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: D82419
                                                                                                                                                                                                           A; Note: sequence extracted from NCBI backbone C; Superfamily: milk fat globule protein; disco
                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A48394; MUID:93250576; PMID:8485470
A;Accession: G48394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine-specific transport protein VCA0772 [imported] - Vibrio cholerae (strain C;Species: Vibrio cholerae C;Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                              A; Experimental source: milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-401 < AOK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
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                                                                            ;Keywords; glycoprotein
;1-32/Domain: EGF homology (fragment) <EG1>
;40-79/Domain: EGF homology <EG2>
;82-239/Domain: discoidin I amino-terminal
;243-401/Domain: discoidin I amino-terminal
                                                                                                                                                                                                                                                                                                                                                          Status: preliminary
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85.7%;
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71.4%;
                                                                                              amino-terminal homology <DN1>
I amino-terminal homology <DN2
  <u>,,</u>
                      Score 30; DB 2;
Pred. No. 1.4e+02;
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Pred. No. 1
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discoidin I amino-terminal
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H.; Dragoi, I.;
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I.; Sellers,
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R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, .; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: F95394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable transmembrane transport protein SMa1937 [imported] - Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #serrence -----
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                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q92Y26; UNIPARC:UPI0000CB2C5; GB:AE006469; A;Experimental source: strain 1021, megaplasmid pSymA A;Experimental source: strain 1021, megaplasmid pSymA R;Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F. pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Ko
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C; Superfamily:
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A;Cross-references: UNIPROT:P79385; UNIPARC:UPI000012F040; EMBL:Y11683; NID:g2652927;
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                                                                                                                                                                                                                                                                              A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-412 < KUR>
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                                                                                                                                                                                                                                                             A; Contents: annotation
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WLISAFA 59
                                         WMLSAFS 7
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ofa domestica (domestic pig)
م المحمد (domestic pig) #text_change 09-Jul-2004
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85.7%;
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1.4e+02
                                                                                                                 .4e+02;
                                                                                                                                    Length 412;
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K.C.
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Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A; Title: Complete genome sequence of a multiple drug resistant A; Reference number: ABO502; MUID:21534947; PMID:11677608
A; A; Ccession: AC0546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Blochem. 240, 628-636, 1996
A;Title: Characterization of glycoprotein PAS-6/7 from membranes of bovine milk fat A;Reference number: S74211; MUID:97008954; PMID:8856064
A;Accession: S74211
A;Molecule type: mRNA
A;Residues: 1-427 <HVA>
                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Kim, D.H.; Kanno, C.; Mizokami, Y.
Biochim. Biophys. Acta 1122, 203-211, 1992
A;Title: Purification and characterization of major glycoproteins, A;Reference number: S23926; MUID:92353107; PMID:1643094
A;Accession: S24181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 19-85;96-110;140-165;174-216;221-232;248-277;285-293;309-337;339-420;425-427
A;Cross-references: UNIPARC:UPI0000177B01; UNIPARC:UPI0000177B02; UNIPARC:UPI0000177B03;
B08; UNIPARC:UPI0000177B09; UNIPARC:UPI0000177B0A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1997 #sequence revision 12-Dec-1997 #text_change
C;Accession: S74211; S78114; S24181; S56138; G48394
R;Hvarregaard, J.; Andersen, M.H.; Berglund, L.; Rasmussen, J.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI000005A272; C;Genetics:
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                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI0000177808
R;Aoki, N.; Kishi, M.; Taniguchi, Y.; Adachi, T.; Nakamura, R.; Matsuda, Biochim. Biophys. Acta 1245, 385-391, 1995
A;Title: Molecular cloning of glycoprotein antigens MGP57/53 recognized A;Reference number: S65138; MUID:96125736; PMID:8541316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: glycoprotein component 16/major fat-globule membrane protein/MFG-E8
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A;Cross-references: UNIPARC:UPI0000177800
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane pro
                                                                                                                   A; Molecule type: mRNA
A; Residues: 27-427 < AOK >
                                                                                                                                                                         A; Status: preliminary; not
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A; Residues: 383-394 < KIM>
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A; Residues: 1-417 < PAR >
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83.3%;
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Pred. No. 1.4e+02;
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e, N.; Farrar,
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membrane proteins,

bovine components 15/16

and

guinea-pig

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A;Reference n
A;Accession:
A;Status: pre
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C,Species: Deinococcus radiodurans
C,Species: Deinococcus radiodurans
C,Date: 03.Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C,Accession: A75444
C,Accession: A75444
R,White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D., M.; Shen, M.; Ventevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zal S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
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F;166-105/Domain: EGF homology <EG2>
F;108-265/Domain: discoidin I amino-terminal homology <DN1>
F;269-427/Domain: discoidin I amino-terminal homology <DN2>
F;269-427/Domain: discoidin I amino-terminal homology <DN2>
F;24-35,29-47,49-58,66-77,71-94,96-105/Disulfide bonds: #status predicted F;27/Binding site: carbohydrate (Ser) (covalent) #status experimental F;34/Binding site: carbohydrate (Thr) (covalent) #status experimental F;99,227/Binding site: carbohydrate (Asn) (covalent) #status experimental F;99,227/Binding site: carbohydrate (Asn) (covalent) #status experimental
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C;Superfamily: milk fat globule protein; discoidin I amino-terminal homology;
C;Keywords: blocked amino end; disulfide bond; glycoprotein; milk
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-427/Product: PAS-6/7 protein #status experimental <MAT>
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A;Molecule type: protein
A;Residues: 233-246 <MAT>
A;Cross-references: UNIPARC:UPI000014C31B
                                                                                              conserved hypothetical protein MYPU_2620 [imported] - Mycoplasma pulmonis (strain UAB C;Species: Mycoplasma pulmonis C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C;Accession: F90544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-454 < WHI>
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, Nucleic Acids Res. 29, 2145-2153, 2001
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma A;Reference number: A99512; MUID:21267165; PMID:11353084
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Pred. No. 1.5e+02;
0; Mismatches 1
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T.; Zalewski,
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submitted to the EMBL Data Library, May 1998 A;Reference number: Z21939 A;Accession: TAGECO
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R;Blanc, V.; Salah-Bey, K.; Folcher, M.; Thompson, C.J.
Mol. Microbiol. 17, 999-999, 1995
A;Title: Molecular characterization and transcriptional
A;Reference number: S70171; MUID:96123441; PMID:8596448
A;Accession: S70171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: MYPU 2620
A;Genetic code: SGC3
C;Superfamily: hypothetical protein MG294
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A;Residues: 1-467 <KUR>
A;Cross-references: UNIPROT:Q98QU9; UNIPARC:UPI00000C8046; GB:AL445566; PID:g14089675;
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-501 <BLA>
A;Cross-references: UNIPROT:Q54806; UNIPARC:UPI00000B6054; EMBL:X84072; NID:g872305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               integral membrane protein - Streptomyces pristinaespiralis
C;Species: Streptomyces pristinaespiralis
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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                                                                                                                                 A; Map position:
                                                                                                                                                                                          A;Cross-references: UNIPROT:O59755; UNIPARC:UPI0000128686; EMBL:AL023587; PIDN:CAA19047.
A;Experimental source: strain 972h-; cosmid c649
                                                                                                                                                                                                                                                 A; Molecule type: DNA
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                                                                                                                                                                                                                                 A;Residues:
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                                    Best Loc
Matches
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;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
;Accession: T40598
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57.1%;
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                                                        Score 30; DB 2;
Pred. No. 1.9e+02;
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Pred. No. 1.7e+02;
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Pred. No. 1.6e+02;
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13

WVLKAFS

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RESULT 50
A39280

Glitamate receptor GluR-II precursor - fruit fly (Drosophila melanogaster)
C.Species: Drosophila melanogaster
C.Species: Drosophila melanogaster
C.Date: 28-Feb-1992 #sequence_revision 10-Apr-1992 #text_change 31-Dec-2004
C.Accession: A39280
C.Accession: A39280
A.Fille: Molecular cloning of an invertebrate glutamate receptor subunit expressed in D
A.Fille: Molecular cloning of an invertebrate glutamate receptor subunit expressed in D
A.Scatcus: preliminary
A.Molecula type: mRNA
A.Scatcus: preliminary
A.Molecula type: mRNA
A.Residues: 1-906 <SCH>
A.Cross-references: UNIPROT:024351; UNIPROT:09VMP4; UNIPARC:UPI0000177962; GB:M73271
C.Genetics:
A.Gene: FlyBase:Glu-RII
A.Gross-references: FlyBase:FBgn0004620
C.Superfamily: mannose 6-phosphate receptor, cation-independent; glutamate receptor F;431-852/Domain: glutamate receptor homology <GRH>
C.Weywords: neurotransmitter receptor
F;431-852/Domain: glutamate receptor homology <GRH>
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Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Matches 5, 20, 20, 20, 66:14:15

Search completed: August 29, 2006, 06:14:15

Search completed: August 29, 2006, 06:14:15
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Scoring table: Sequence: Title: Perfect score: Run on: OM protein - protein search, using sw model August 29, 2006, 05:47:27; Search time 56 Seconds (without alignments) 115.627 Million cell updates/sec US-10-541-343-3 38 BLOSUM62 WMLSAFS 7 Copyright GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd. 2 32 84 187

Total number of hits satisfying chosen parameters: Searched: 2849598 seqs, 925015592 residues

Gapop 10.0 , Gapext 0.5

Minimum Maximum DB BB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database UniProt\_7.2:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Q3jk96 Q6k6i3

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Q6za46 Q6c2l1 Q4bh19

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Q7wbe3 Q7vux6 P28935

Q6s6p9

Q2tnu0 Q2tnu1 Q2tnu4 Q35c16 Q8z0p0 Q9kal1 Q7wmw4

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Distributed under the Creative Commons Attribution-NoDerivs L  EMBL; AN172685; AAO.18202.1; -; Genomic_DNA.  Hypothetical protein; Plasmid.  SEQUENCE 71 AA; 7742 MW; DF8FD8708D007D11 CRC64;  Query Match  92.1%; Score 35; DB 2; Length 71;  Best Local Similarity 85.7%; Pred. No. 15;  Matches 6; Conservative 1; Mismatches 0; Indels 0  1 MMLSAFS 7    :    58 MMVSAFS 64	NUCLEOTIDE SEQUENCE.  STRAIN=ATCC 31832; MEDLINE=22830013; PubMed=12948627; DOI=10.1016/S0168-1656(03) Tauch A., Puhler A., Kalinowski J., Thierbach G.; "Plasmids in Corynebacterium glutamicum and their molecular classification by comparative genomics."; J. Biotechnol. 104:27-40(2003).  Copyrighted by the UniProt Consortium, see http://www.uniprot	SULT 1 4GE6 CORGL QB4GE6 CORGL QB4GE6 CORGL QB4GE6 O1-JUN-2003, integrated into UniProtKB/TrEMBL. O1-JUN-2003, sequence version 1. O7-FEB-2006, entry version 11. Hypothetical protein. Corynebacterium glutamicum (Brevibacterium flavum Plasmid pCG2. Bacteria, Actinobacteria; Actinobacteriaceae; Corynebact NCBI TaxID-1718;	ALIGNMENTS  ALIGNMENTS	94 29 76.3 356 2 Q8Y4A1 LISMO Q8Y4A1 95 29 76.3 356 2 Q4S6D4 TETING Q4S6D4 96 29 76.3 361 2 Q8S2F4 TRYSA Q8S2F4 97 29 76.3 363 2 Q8FHX9 ECOL6 Q8fhx9 98 29 76.3 365 2 Q397L4_BURS3 Q397L4 99 29 76.3 367 2 Q4BLVO BURVI Q45bVO Q397L4	89 29 76.3 351 2 Q9LFW3 ARAFH  89 29 76.3 351 1 NUZM PĀRLI  90 29 76.3 352 1 NUZM PĀRLI  91 29 76.3 354 2 Q2SOZO 9SPHI Q2SOZO  92 29 76.3 354 2 Q6SX78 Q8VSA  93 29 76.3 356 2 Q4EMX4_LISMO Q4emx4	83 29 76.3 342 2 Q2TNS9_DDIPT Q2tns9 84 29 76.3 346 2 Q649H8 9ARCH Q649h8 85 29 76.3 347 2 Q95XT7 ARATH Q9545h7 86 29 76.3 348 2 Q59IV6_MESCR Q59IV6 87 29 76.3 349 2 Q35GT0_ARATH Q36CN Q	72 29 76.3 335 2 Q53GOO HUMAN Q53900 73 29 76.3 335 2 Q9HOU3 HUMAN Q9HOU3 74 29 76.3 335 2 Q8HBU6 HUMAN Q8hbh6 75 29 76.3 335 2 Q5RE31 PONPY Q5re31 76 29 76.3 335 2 Q5RE31 PONPY Q5re31 77 29 76.3 335 2 Q9CCY5 MOUSE Q9ccY5 77 29 76.3 335 2 Q9CZY3 MOUSE Q9cCY5 78 29 76.3 335 2 Q9CZY3 MOUSE Q9cCY5 79 29 76.3 339 2 Q7B798 PSEAE Q7b798 79 29 76.3 339 2 Q7B798 PSEAE Q7b798 80 29 76.3 342 2 Q6DU8 PERFU 81 29 76.3 342 2 Q5TNRS 9DIPT Q2cnrs 82 29 76.3 342 2 Q5TNRS 9DIPT Q2cnrs	70 29 76.3 335 1 BTUC PHOLL Q7n3q3 71 29 76.3 335 1 IAGZ_RAT Q35777
Distributed under the Creative Commons Attribution-NoDerivs L  EMBL; AN172685; AAO.18202.1; -; Genomic_DNA.  Hypothetical protein; Plasmid.  SEQUENCE 71 AA; 7742 MW; DF8FD8708D007D11 CRC64;  Query Match  92.1%; Score 35; DB 2; Length 71;  Best Local Similarity 85.7%; Pred. No. 15;  Matches 6; Conservative 1; Mismatches 0; Indels 0  1 MMLSAFS 7    :    58 MMVSAFS 64	NUCLEOTIDE SEQUENCE. STRAIN=ATCC 31832; MEDLINE=22830011; PubMed=12948627; DOI=10.1016/S0168-1656(03) Tauch A., Publer A., Kalinowski J., Thierbach G.; "Plasmids in Corynebacterium glutamicum and their molecular classification by comparative genomics."; J. Biotechnol. 104:27-40(2003). Copyrighted by the UniProt Consortium, see http://www.uniprot	SULT 1 4GE6 CORGL Q84GE6 CORGL PRELIMINARY; PRT; 71 AA. Q84GE6; O1-JUN-2003, integrated into UniProtKB/TrEMBL. O1-JUN-2003, sequence version 1. O7-FEB-2006, entry version 11. Hypothetical protein. Corynebacterium glutamicum (Brevibacterium flavum). Plasmid pCG2. Bacteria; Actinobacteria; Actinomycetales Corynebacterineae; Corynebacteriaceae; Corynebacterium. NCBI TaxID-1718;	00 29 76.3 368 2 Q2ULU3_ASFOR Q2ULJ3	94 29 76.3 356 2 Q8Y4A1 LISMO Q8Y4A1 listeria 95 29 76.3 356 2 Q4S6D4 TEYING Q4S6D4 tetraodon 96 29 76.3 361 2 Q8S2F4 TRYSA Q8S2F4 oryza sat 97 29 76.3 363 2 Q8FHX9 ECOL6 Q8fhx9 escherich 98 29 76.3 365 2 Q397L4_BURS3 Q397l4 burkholde 99 29 76.3 367 2 Q4BLVO BURVI Q45LVO burkholde 99 29 76.3 367 2 Q4BLVO BURVI Q45LVO burkholde	89 29 76.3 351 2 Q9LFW3 ARAFH  89 29 76.3 351 1 NUZM PĀRLI  90 29 76.3 352 1 NUZM PĀRLI  91 29 76.3 353 2 Q2SOZO 9SPHI Q2SOZO  92 29 76.3 354 2 Q6SXZO QXXXA  93 29 76.3 356 2 Q4EMX4_LISMO Q4emx4	83 29 76.3 342 2 Q2TNS9_DIPT Q2tns9 84 29 76.3 346 2 Q649H8 9ARCH Q649h8 85 29 76.3 347 2 Q954V7_ARATH Q954Y0 86 29 76.3 348 2 Q59IV6_MESCR Q59IV6 87 29 76.3 348 2 Q59IV6_MESCR Q59IV6 88 29 76.3 349 2 Q3E6TO_ARATH Q59IV6	72 29 76.3 335 2 Q53GO HUMAN Q53gOU 73 29 76.3 335 2 Q9HOU3-HUMAN Q9hOu3 74 29 76.3 335 2 Q8NBNG HUMAN Q8nbn6 75 29 76.3 335 2 Q8NBNG HUMAN Q8nbn6 76 29 76.3 335 2 Q5RE31_PONPY Q5re31 76 29 76.3 335 2 Q9CCY5_MOUSE Q9ccY5 77 29 76.3 335 2 Q9CCY5_MOUSE Q9ccY5 77 29 76.3 335 2 Q9CZT3_MOUSE Q9czY5 78 29 76.3 339 2 Q7B798_PSEAE Q7b798 79 29 76.3 339 2 Q7B798_PSEAE Q7b798 80 29 76.3 342 2 Q6BDU8_PERFU 81 29 76.3 342 2 Q5BDU8_PERFU 82 29 76.3 342 2 Q5BDU8_PERFU 83 29 76.3 342 2 Q5BU8_PERFU 84 29 76.3 342 2 Q5BU8_PERFU 85 29 76.3 342 2 Q5BU8_PERFU 86 29 76.3 342 2 Q5BU8_PERFU 87 29 76.3 342 2 Q5BU8_PERFU 88 29 76.3 342 2 Q5BU8_PERFU 89 76 3 342 2 Q5BU8_PERFU 80 29 76.3 342 2 Q5BU8_PERFU 80 29 76.3 342 2 Q5BU8_PERFU 81 29 76.3 342 2 Q5BU8_PERFU 82 29 76.3 342 2 Q5BU8_PERFU 83 29 76.3 342 2 Q5BU8_PERFU 84 29 76.3 342 2 Q5BU8_PERFU 85 29 76.3 342 2 Q5BU8_PERFU 86 29 76.3 342 2 Q5BU8_PERFU 87 29 76.3 342 2 Q5BU8_PERFU 88 20 76.3 342 2 Q5BU8_PERFU 89 20 76.3 342 2 Q5BU8_PERFU 90 20 20 20 20 20 20 20 20 20 20 20 20 20	70 29 76.3 335 1 BTUC PHOLL Q7n3q3 photo 71 29 76.3 335 1 IAGZ_RAT 035777 rattu

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Q8N0ZO H

AC Q8N0ZO H

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DT 01-OCT-2

DT 07-FEB-2

DC CONCLETTAX

RN NUCLEOTI

RA SUWA M.,

RA TSUTSUMI

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CO GO:0

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GO; GO:00
GO; GO:00
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Q5L241;
Q1-FEB-2005, integrated into U
01-FEB-2005, sequence version
07-FEB-2006, entry version 6.
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PROSITE; PS00980; G_PROTEIN_RECEP_F3_3;
PROSITE; PS00981; G_PROTEIN_RECEP_F3_4;

PROSITE; PS50259; G_PROTEIN_RECEP_F3_4;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0008067; F:metabotropic glutamate, GA
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR000337; GPCR Mgr.
InterPro; IPR011500; NCD3G_GPCR.
                                                                                         PubMed=15576355; DOI=10.1093/nar/gkh970;
Takami H., Takaki Y., Chee G.-J., Nishi
Matsui S., Uchiyama I.;
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01-OCT-2002,
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                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                             Geobacillus kaustophilus
                                                                                                                                                                                                                                                                                                           OrderedLocusNames=GK0704;
                                                                                                                                                                                                                                                                                                                               Maltose/maltodextrin transport system (Subsrate-binding protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seven transmembrane helix receptor.
                                               "Thermoadaptation trait revealed by the thermophilic Geobacillus kaustophilus.";
                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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                           Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00003; 7tm_3; PF07562; NCD3G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB065450; BAC05713.1; -; Genomic_DNA.
AB065566; BAC05802.1; -; Genomic_DNA.
AB065486; BAC05739.1; -; Genomic_DNA.
                           Acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENSG00000198822; Homo sapiens.
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                        Res. 32:6292-6303(2004)
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                                                                                                                                                                                         [LARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.1%;
85.7%;
                                               kaustophilus.";
                                                                                                                                                                                         SCALE GENOMIC DNA
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Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                          얁
                                                                                                                    Suzuki
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                                                                R GO; GO:0005739; C:mitochondrion; IEA.

R GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA

R GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0042773; P:ATP synthesis coupled electron transport; IEA

R GO; GO:0006120; P:mitochondrial electron transport, NADH to u.

R InterPro; IPR003918; NADHub oxred4.

R InterPro; IPR010227; NDH I M.

R InterPro; IPR010227; NDH Z M.

R InterPro; IPR000260; Oxidored q1.

R InterPro; IPR000260; Oxidored q5.

R PANNHER; PTHR11460; NADHub oxred4; 1.

R Pfam; PF03051; Oxidored q5. N; 1.

R Pfam; PF01059; Oxidored q5. N; 1.

R Pfam; PF01059; Oxidored q5. N; 1.

R PRINTS; RR01437; NUOXDRDTASE4.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.

MEDLINE=21097353; PubMed=11161749; DOI=10.1006/mpev.2000.0870;

MOUCHATY S.K., Catzeflis F., Janke A., Arnason U.;

"Molecular evidence of an African Phiomorpha-South American
Caviomorpha clade and support for Hystricognathi based on the
mitochondrial genome of the came rat (Thryonomys swinderianus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Hystricognathi; Thryonomyidae; Thryonomys.
NCBI_TaxID=10169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0006810; P:transport; IEA.
InterPro; IPR006060; Maltose_bd.
InterPro; IPR006059; SBP_bac_1.
InterPro; IPR006059; SBP_domI.
Pfam; PF01547; SBP_bac_1; 1.
PRINTS; PR00181; MĀLTOSĒBP.
PROSITE; PS01037; SBP_BACTERIAL_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GG; GO:0005363; F:maltose transporter ac
GO; GO:0005215; F:transporter activity;
GO; GO:0015768; P:maltose transport; IE:
GO; GO:0006810; P:transport; IEA.
PRINTS; PR0143/; NOW. I PRINTS; PR0143/; NOW. I TIGREAMS; TIGR01972; NDH I M; 1.

Mitochondrion; NAD; Oxidoxeductase; Ubiquinone.

Mitochondrion; NAD; S1966 MW; E6DD0150CC0C9F56 CRC64;
                                                                                                                                                                                                                                                                                                                                                         Mol. Phylogenet. Evol. 18:127-135(2001).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+)
-!- SIMILARITY: Belongs to the complex I subunit 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dehydrogenase subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NADH-ubiquinone oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001, sequence version 07-FEB-2006, entry version 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001, integrated into UniProtKB/TrEMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9B6F3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome. SEQUENCE 424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thryonomys swinderianus (Greater cane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=NADH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9B6F3
                                                                                                                                                                                                                                                                                                              Distributed under the Creative Commons Attribution-NoDerivs License
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O:0005363; F:maltose transporter activity; IEA.
                                                                                                                                                                                                                                                                             AJ301644; CAC27808.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P:maltose transport; IEA.
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain 4 (EC 1.6.5.3) (NADH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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92;
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family.
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RESULT OF STREET OF STREET
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                                                                                                                                                                                                                                                                      Addms N.D., Celniker S.E., Holt R.A., Evens C.A., Gocayme J.D., RA Adams N.D., Celniker S.E., Hil P.W., Hoskins R.A., Golayme J.D., RA Admanatides P.G., Scherer S.E., Hil P.W., Hoskins R.A., Galle R.F., RA Admanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Barli J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D., RA Barli J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D., RA Barli J.F., Basu A., Basxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolthakov S., RA Borkova D., Botchan M.R., Bouck J., Barkaterin P., Brottier P., Ra Borkova D., Botchan M.R., Bouck J., Barkaterin P., Brottier P., Ra Borkova D., Botchan M.R., Bouck J., Barkaterin P., Brottier P., Chandra I., RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dukov B.C., Dunn P., RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dukov B.C., Dunn P., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Holtin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Alasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Baceb M.G., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Merkulov G., Sielen-Kiamos I., Simpson M., Skupski M.P., Smith T., Shen H., Shue B.C., Sielen-Kiamos I., Simpson M., Skupski M.P., Smith T., Ra Ra Ra Merkulov G., Stepleton M., Strong R., Wang X., Yao Q.A., Yeng S., Yao Q.A., Wang S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches 6
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Q9VLT3;
01-MAY-2000, i
                                  George R.A.,
Pacleb J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2006, entry version 32. CG7586-PA (LD23292p). Name=MCr; ORFNames=CG7586, Dmel.
                                  Celniker S.B., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE, PUMEDLINE=20196006; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neoptera; Endopterygota; Dip
Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
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                                                                                                                                                                 MEDLINE=22426065;
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                                                                                                                                                                                                                                                             287:2185-2195(2000).
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Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                              PubMed=12537568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=10731132; DOI=10.1126/science.287.
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               Stapleton
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               G.G.,
                                                                                                                                    Halpern
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С.,
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FlyBase; FBgn0020240; Mcr.
GO; GO:0005515; F:protein binding; If
InterPro; IPR011626; A2M_comp.
InterPro; IPR002890; A2M_N.
InterPro; IPR011625; A2M_N.
InterPro; IPR011627; A2M_rcpt.
InterPro; IPR001599; MacrogloblnA2.
InterPro; IPR001599; MacrogloblnA2.
Pfam; PF00207; A2M; 1.
Pfam; PF07678; A2M comp; 1.
Pfam; PF07635; A2M N; 1.
Pfam; PF071635; A2M N 2; 1.
Pfam; PF07677; A2M recep; 1.
Pfam; PF00057; Ldl recept a; 1
SMART; SM00192; LDLa; 1.
PROSITE; PS50068; LDLAA 2; 1.
SEQUENCE 1760 AA; 202783 MW
                                                                                                                                                                                                                                                                                                                                                      Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J. Champe M., Chavez C., Dorsett V., Farfan D., Frise E., Georg Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Yu C., Levis S.E., Rubin G.M., Celniker S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S. Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman E Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Celniker S., Carlson of Hoskins R., Stapleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ashburner M., Celniker S.E.
"The transposable elements
a genomics perspective.";
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MEDITINE=22426070; PubMed=12537573;
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Genome Biol.
                                                                                                                                                                                                                                                              EMBL; AE003619; AAF52601.1; EMBL; AY058526; AAL13755.1;
                                                                                                                                                                                                                                                                                                                                                Submitted
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MEDLINE=22426069; PubMed=12537572;
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S., Carlson J., Wan K., Pfeiffer
R., Stapleton M., Pacleb J., Park
                                                                                                                                                                                                                                                                                                                                               (OCT-2001) to the EMBL/GenBank/DDBJ
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er euchromatic genome sequence.";
1. 3:RESEARCH0079-RESEARCH0079(2002).
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     B8E0602350E87F86 CRC64;
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M., Rubin G.M.,
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02-AUG-2005,
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07-FEB-2006,
Non-specific |
antioxidant p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavin. Hammon N., Israni S., Pitluck S., Richardson P.; "Sequencing of the draft genome and assembly of Rhodopseudomonas palustris BisBl8."; Submitted (OCT-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid adenylation. ORFNames=RPCDRAFT_2142;
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GO:0030170; F:pyridoxal phosphate binding;
GO:0008483; F:transaminase activity; IEA.
GO:0016740; F:transferase activity; IEA.
GO:0016633; P:fatty acid biosynthesis; IEA.
GO:0008152; P:metabolism; IEA.
GO:0008152; P:metabolism; IEA.
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                                                                                                                                                                                                                                                                                                                                                                               preliminary data.
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Hoffmaster A.R., Ravel J., Rasko D.T., Fitzgerald C., Mayer
Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer
Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.
Maiden J., Peterson S.N., Weyant R.S., Galloway D.R., F
                                                                                                                                                                                                                                                                                                                                                                                                             Name=dps; OrderedLocusNames=BCE3JL1825; Bacillus cereus (strain ZK / E3JL).
Bacteria; Firmicutes; Bacillales; Bacillacillus cereus group.
NCBI TaxID=288681;
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"Identification of anthrax toxin genes in a Bacillus with an illness resembling inhalation anthrax.";
Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
-!- CAUTION: The sequence shown here is derived from the control of t
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                               EMBL;
                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
Brettin T.S., Bruce D., Challacombe J.F., Gilna
Hitchcock P., Jackson P., Keim P., Longmire J.,
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ProDom; PD149803; DPS; 1.
PROSITE; PS00818; DPS_1; 1.
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Hitchcock P., Jackson P., Keim P.
Richardson P., Rubin E., Tice H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0006879; P:iron ion homeostasis; GO; GO:0006950; P:response to stress; InterPro; IPR002177; DPS_DNA_bd.
                                                                                                                                                                                             "Complete genome sequence of Bacillus cereus ZK.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G0:0003677; F:DNA binding;
G0:0003677; F:DNA binding;
G0:000819; F:ferric iron l
G0:0006879; P:iron ion home
G0:0006950; P:response to a
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   Q63CE7;
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                               CP000001; AAU18426.1;
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                                                                                             iProt Consortium, see http://www.uniprot.org/to
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                                  Genomic_DNA
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                                                                                                                                                                                                                                                                                                  Okinaka
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GO; GO:0008199; F:ferric iron binding; IEA.
GO; GO:0004322; F:ferroxidase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016490; P:iron ion homeostasis; IEA.
GO; GO:0006879; P:iron ion bomeostasis; IEA.
GO; GO:0006890; P:response to stress; IEA.
InterPro; IPR002177; DPS_DNA_bd.
InterPro; IPR002177; DPS_DNA_bd.
InterPro; IPR002331; Ferritin_Dps.
InterPro; IPR002331; Ferritin_rel.
Pfam; PF00210; Ferritin; 1.
                                                                                         Pfam; PF00210; Ferritin; 1.
Pfam; PF00210; Ferritin; 1.
PR.NTS; PR01346; HELNAPAPROT.
ProDom; PD149803; DPS; 1.
PROSITE; PS00818; DPS; 1; 1.
PROSITE; PS00818; DPS; 1; 1.
                                                                                  Complete
SEQUENCE
                                                                                                                                                                                                           Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S. Richardson P., Rubin E., Tice H.; Longmire J., Edge S. "Complete genome sequence of Bacillus thuringiensis 97-2 Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-2004, integrated into UniProtKB/Tv
19-JUL-2004, sequence version 1.
07-FEB-2006, entry version 14.
Non-specific DNA-binding protein Dps (EC
Name-dps; OrderedLocusNames-BT9727 1841;
Baccillus thuringiensis subsp. konkukian.
Bacteria; Firmicutes; Bacillales; Bacilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01346; HELNAPAPROT.
ProDom; PD149803; DPS; 1.
PROSITE; PS00818; DPS 1; 1.
Complete proteome; DNA-binding;
                                                                                                                                                              InterPro; IPR002177; DPS_DNA_bd.
InterPro; IPR008331; Ferritin_Dps.
InterPro; IPR012347; Ferritin_rel.
                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=97-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=180856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus cereus group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q6HJV3;
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                                                                                                                                                                                                                     L; AE017355; AAT63428.1; -; Genomic_DNA.; Q6HJV3; 2-147.
GO:0003677; F:DNA binding; IEA.
GO:0008199; F:ferric iron binding; IEA.
GO:0004322; F:ferroxidase activity; IEA.
GO:0016491; F:oxidoreductase activity; IIEA.
GO:0006879; P:iron ion homeostasis; IEA.
                                                                                                                                                                                                         GO:0006879; P:iron ion homeostasis; IE GO:0006950; P:response to stress; IEA.
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                         6; Conserv
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                                                                                proteome;
147 AA;
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147 AA;
                         89.5%; ilarity 100.0%; Conservative
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                                                                                  16707 MW;
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                            0,
                                        Score 34;
Pred. No.
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                                                                                Oxidoreductase.
2745255C84FCCCCD CRC64;
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                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillaceae; Bacillus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y; IEA.
v; IEA.
v; IEA.
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                                        DB 2;
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S., Okinaka F
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RESULT 11
Q739P8 BACC1
Q739P8 BACC1
D7 Q739P8;
AC Q739P8;
DT 05-JUL-2004, integrated into
D7 05-JUL-2006, entry version
D7 07-MAR-2006, entry version 14
DE General stress protein.
GN Name-dps; ORFNames=BCE 2002;
OS Bactllus Cereus (strain ATCC
OC Bacteria; Firmicutes; Bacilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q813P2_BACCR
ID Q813P2_DACCR
ID Q813P2_DT
O1-JUN-2
DT O1-FEB-2
DT O1-JUN-2
DT O1-FEB-2
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01-JUN-2003, integrated into UniProtKB/TrEMBL.

01-JUN-2003, sequence version 1.

07-FEB-2006, entry version 18.

Non-specific DNA-binding protein Dps / Iron-binding ferritin-like

antioxidant protein / Ferroxidase (EC 1.16.3.1).

OrderedLocusNames=BC2011; ORFNames=BC_2011;

Dacillus cereus (strain ATCC 14579 / DSM 31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01346; HELNAPAPROT.
ProDom; PD149803; DPS; 1.
PROSITE; PS00818; DPS; 1.
Complete proteome; DNA-binding;
SEQUENCE 147 AA; 16680 MW; 3
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MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;

Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,

Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,

Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,

Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,

Overbeek R., Kyrpides N.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BioCyc; BCER226900.BC2011-MONOMER; -. GO; GO:0003677; F:DNA binding; IEA. GO; GO:0008199; F:ferric iron binding; IEA. GO; GO:0004322; F:ferroxidase activity; IEA. GO; GO:0006479; F:oxidoreductase activity; IEA. GO; GO:0006879; P:ixon ion homeostasis; IEA. GO; GO:0006879; P:response to stress; IEA. GO; GO:0006950; P:response to stress; IEA.
      Name=dpS; ORFNames=BCE 2092;
Bacillus cereus (strain ATCC 10987)
Bacteria; Firmicutes; Bacillales; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002177; DPS_DNA_bd.
InterPro; IPR008331; Ferritin_Dps.
InterPro; IPR012347; Ferritin_rel.
Pfam; PF00210; Ferritin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; Q8RPQ1; 1JIG.
SMR; Q813P2; 2-147.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=226900;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 423:87-91(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus cereus group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                             sequence version
                                                                                                                                                                                          integrated into UniProtKB/TrEMBL
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Pred. No.
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36A4D54D650CCCCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
            Bacillaceae;
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            Bacillus;
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RESULT OBREPOLT ID POLT OF REPOLT OF
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Best Local
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GenomeReviews; AE017194 GR; dpS.
GO; GO:0008199; F:ferric iron binding; 1
GO; GO:0006879; P:response to stress; II
GO; GO:0006950; P:response to stress; II
InterPro; IPR002177; DPS DNA bd.
InterPro; IPR008331; Ferritin_Dps.
InterPro; IPR012347; Ferritin_rel.
MEDIINE=22608414; PubMed=12721629; DOI=10.1038/nature01586; Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T. Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Melson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L., Endowy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., DeBoy R.T., Madgu R., Daugherty S.C., Durkin A.S., Radune D., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F., Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OBRPQ1 BACAN PRELIMINARY; PRT; 147 AA.
Q8RPQ1; Q6HZV3; Q6KTT5; Q81RM9;
Q1-JUN-2002, integrated into UniProtKB/TrEMBL.
O1-JUN-2002, sequence version 1.
O7-MAR-2006, entry version 25.
Miniferritin Dlp2 (General stress protein).
Name=dlp2; Synonyms=dpS; OrderedLocusNames=BA2013,
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SMR; Q739P8; 2-147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01346; HELNAPAPROT.
ProDom; PD149803; DPS; 1.
PROSITE; PS00818; DPS_1; 1.
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MEDLINE=21964043; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes;
Bacillus cereus group.
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NCBI_TaxID=222523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1392
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                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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J. Biol. Chem. 27
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BACAN
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                                                                                                                                                                                                                                                                                                                                                        isolate Porton;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wo iron-binding proteins 277:15093-15098 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11836250;
don W.G., Pitulis
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100.0%; Pred. No.
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on homeostasis; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOI=10.1074/jbc.M112378200;
N., Battistutta R., Montecu
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51;
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lonay J.F.,
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RESULT 13
Q3EXQ4 BACTI
ID Q3EXQ4;
AC Q3EXQ4;
DT 08-NOV-2
DT 07-PEB--
DE NON-SPE
DE NON-SPE
DE ARTIOXAIG
GN ORFNAMES
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Best Local S
Matches 6
                                                                              OJEXQ4 BACTI PRELIMINARY; PRT; 154 AA.
OJEXQ4;
OB-NOV-2005, integrated into UniProtKB/TrEMBL.
OB-NOV-2005, sequence version 1.
O7-FEB-2006, entry version 3.
Non-specific DNA-binding protein Dps / Iron-bind antioxidant protein / Ferroxidase (EC 1.16.3.1).
ORFNames=RBTH 06140;
Bacillus thuringiensis serovar israelensis ATCC.
          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus cereus group.

MCBI TaxID=339854;

[11]
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GenomeReviews; AE016879_GR; BA2013.
GenomeReviews; AE017225_GR; BAS1871.
GenomeReviews; AE017334_GR; GBAA2013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of Bacillus anthracis Submitted (JAN-2004) to the EMBL/GenBank/DDBJ da
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brettin T.S., Bruce D., Challacom
Hitchcock P., Jackson P., Keim P.
Richardson P., Rubin B., Tice H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-2004) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson M., S
Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The genome sequence of Bacillus anthracis closely related bacteria.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 147 AA
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ProDom; PD149803; DPS; 1.
PROSITE; PS00818; DPS_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sterne;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Bacillus anthracis comparative submitted (MAY-2004) to the EMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00210; Ferritin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0006879; P:iron ion homeost; GO; GO:0006950; P:response to stre: GO; GO:0006950; P:response to stre: InterPro; IPR002177; DPS DNA bd. InterPro; IPR008331; Ferritin_ps. InterPro; IPR012347; Ferritin_rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0008199; F:ferric iron binding; GO:0006879; P:iron ion homeann GO:0006879;
                                                                                                                                                                                                                                                                                                                                                          140
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AE016879; AAP25903.1; -;
AE017225; AAT54186.1; -;
AE017334; AAT31135.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423:81-86(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 100.0%; 6; Conservative (
                                                                                                                                                                                                                                                                                                                                                            WMLSAF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cline R.T., Redmond C.,
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GG; GC:0003677; F:DNA binding; IEA.
GG; GC:00008199; F:ferric iron binding
GG; GC:00008192; F:ferroxidase activi
GG; GC:0004322; F:ferroxidoreductase activi
GG; GC:0006491; F:oxidoreductase activi
GG; GC:0006879; P:iron ion homeostas;
GG; GC:0006879; P:response to stress
                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

PubMed=15703294; DOI=10.1073/pnas.0409900102;

Ruby E.G., Urbanowski M., Campbell J., Dunn A., Faini M.,

Lostroh P., Lupp C., McCann J., Millikan D., Schaefer A.,

Stevens A., Visick K., Mistler C., Greenberg E.P.;

"Complete genome sequence of Vibrio fischeri: a symbiotic
with pathogenic congeners.";
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"Comparative rose"
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15-MAR-2005, integrated into 1
15-MAR-2005, sequence version
07-FEB-2006, entry version 5.
EMBL; CP000020; AAW85552.1; -; Genomic_DNA. GO; GO:0016020; C:membrane; IEA. GO; GO:0005293; F:lysine permease activity; GO; GO:0006865; P:amino acid transport; IEA
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InterPro; IPR002331; Ferritin_Dps.
InterPro; IPR012347; Ferritin_rel.
Pfam; PF00210; Ferritin; 1.
                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprodistributed under the Creative Commons Attribution-NoDerivs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrio fischeri (strain ATCC 700601 / ES114).
Bacteria; Proteobacteria; Gammaproteobacteria;
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Probom; PD149803; DPS; 1.
PROSITE; PS00818; DPS; 1; 1.
PROSITE; PS00818; DPS; 1; 1.
DNA-binding; Oxidoreductase.
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                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009(2005)
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GO:0008199; F:ferric iron binding; IEA
GO:0004322; F:ferroxidase activity; IE
GO:0016491; F:oxidoreductase activity;
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Q2W9C2_MAGSA
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Best Local S
Matches 6
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Best Local
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Pfam; PF01810; LysE; 1
Complete proteome.
SEQUENCE 211 AA; 22
                                                                                                                                                                                                                                                                                      QZW9C2 MAGSA
QZW9C2;
10-JAN-2006,
10-JAN-2006,
07-MAR-2006,
    "Complete
Bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OrderedLocusNames=MAP0370; ORFNames=MAP_0370;
                                                         PubMed=16303747;
Matsunaga T., Okamura
                                                                                                      STRAIN=AMB-1
                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                                                                                                              NCBI_TaxID=342108;
                                                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria;
Rhodospirillaceae; Magnetospirillum.
                                                                                                                                                                                                         Magnetospirillum magneticum
Bacteria; Proteobacteria; Al
                                                                                                                                                                                                                                                    ORFNames=amb0749;
                                                                                                                                                                                                                                                                     Permease of the major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE016958; AAS02687.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li L., Bannantine J., Zhang Submitted (SEP-2003) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium paratuberculosis
                                          Takeyama H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR005614; NrfD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteome; Hypothetical 361 AA; 37516 MW; 9
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Genome Sequence of Magnetospirillum sp
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                                                                                                                                                                                                                                                                                           entry version 4.
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                                                              Fukuda Y.,
  sp.
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EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34;
Pred. No.
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                                                                                                                                                                                                                                 AMB-1
  the Facultative
p. strain AMB-1."
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Pred. No. 1
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                                                              Wahyudi A.T.,
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73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3e+02;
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                                                                Murase Y.,
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Q44233
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P88944
ID P88947
AC P8
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Best Local
P88944;
01-MAY-1997, integrated into UniProtKB/T
01-MAY-1997, sequence version 1.
07-FEB-2006, entry version 23.
0RF 56 (DNA replication protein).
Human herpesvirus 8 (HHV-8) (Kaposi's salviruses; dsDNA viruses, no RNA stage; He Gammaherpesvirinae; Rhadinovirus.
NCBI_TaxID=37296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 ARTSP
Q44233 ARTSP
Q44233;
Q1-NOV-1996,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.

MEDLINE=95238267; PubMed=7721689;

Gutshall K.R., Trimbur D.E., Kasmir J.J., Brenchley J.E.;

"Analysis of a novel gene and beta-galactosidase isozyme:
psychrotrophic Arthrobacter isolate.";

J. Bacteriol. 177:1981-1988(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U17417; AAA75601.1; -; Genomic_DNA.
GO; GO:0009341; C:beta-galactosidase complex; IEA.
GO; GO:0004565; F:beta-galactosidase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR003476; Glyco_hydro_42.
Pfam; PF02449; Glyco_hydro_42; I.
PIRSF; PIRSF001084; B-galactosidase; 1.
SEQUENCE 637 AA; 70895 MW; 98160B4FCC3A728C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Micrococcaceae; Arthrobacter.
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07-FEB-2006, entry version 20.
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                                                                                                                                                                                                             4_HHV8
P88944_HHV8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1667;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
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SUBCELLULAR LOCATION:
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membrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by the UniProt Consortium, under the Creative Commons
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AA; 48181
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85.7%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 2;
Pred. No. 2.3e+02;
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                                                                                                                                                                                                                  843 AA
                                                    Herpesviridae;
                                                                        sarcoma-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA.
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Attribution-NoDerivs License
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1.6e+02;
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                                                                           herpesvirus)
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RESULT 19
Q3WYR2_9ACTN
ID Q3WYR2;
AC Q3WYR2;
DT 11-OCT-2005, EDT 11-OCT-2005, EDT 07-MAR-2006, EDT VAly1-tRNA Sylen
DT VAly1-tRNA Sylen
CO RUMONDACTER RAYIT
OC RUMONDACTER RAYIT
OC RUMONDACTER RAYIT
OC RUMONDACTER RAYIT
OX NCBI_TAXID=266
RN [1]
RP NUCLEOTIDE SECULATION SECUL
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U75698; AAC57138.1; -; Genomic_DNA.
EMBL; U93872; AAB62614.1; -; Genomic_DNA.
GO; GO:0003896; F:DNA primase activity; IEA.
GO; GO:0006260; P:DNA replication; IEA.
InterPro; IPR004340; UL52 UL70.
Pfam; PF03121; Herpes_UL52; 1.
SPONIENCE 843 AA; 95554 MW; 89248BFCB7DB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIJINE=7/27/22... Pleckensus... Neipel F., Albrecht J.-C., Fleckensus... "Cell-homologous genes in the Kaposi's sa "Cell-homologous genes in the Kaposi's sa
                                                                                                                                                                                                                  Valyl-tRNA synthetase, class Ia.
ORFNames=RxylDRAFT_0191;
Rubrobacter xylanophilus DSM 9941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neipel F., Albrecht J.-C., Ensser A., Huang Y. Friedman-Kien A.E., Fleckenstein B.; Friedman-Kien A.E., Fleckenstein B.; With genome of human herpesvirus 8 cloned from Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parry J.P., Peruzzi D.,
Submitted (MAY-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes by KSHV."
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     US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K.,
Hammon N., Israni S., Pitluck S., Richardson
                                                                                                                                                                                                                                                                                      11-OCT-2005, integrated into t
11-OCT-2005, sequence version
07-MAR-2006, entry version 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
MEDLINE=97296220; PubMed=9151804;
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Russo J.J., Bohenzky
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                                                                                                                                           Rubrobacterineae; | NCBI_TaxID=266117;
                                                                                                                                                                            Bacteria; Actinobacteria; Rubrobacteridae; Rubrobacterales;
Rubrobacterineae; Rubrobacteraceae; Rubrobacter.
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Parry J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97121480; PubMed=8962146; DOI=10.1073/pnas.93.25.14862;
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                                                                           STRAIN=DSM 9941;
                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Distributed
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rol. 71:4187-4192(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by the UniProt Consortium, see http://www.uniprot.org/terms under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                         Rubrobacteraceae;
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Pred. No.
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       Detter P.;
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RESULT 20
Q73RB9_TREDE
ID Q73RB9_TREDE
AC Q73RB9;
DT 05-UUL-2004, i
DT 05-UUL-2004, i
DT 05-UUL-2006, e
DT 07-MAR-2006, e
DT Nuclease SbcCl
GN OrderedLocusNa
OS Treponema dent
OC Bacteria; Spin
OX NCBI_TaxID=156
RN [1]
OX NCBI_TAXID=166
RO STRAIN=ATCC 35
RX PubMed=1506438
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Best Local
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05-JUL-2004, sequence version
07-MAR-2006, entry version 20.
Nuclease SbCCD, C subunit, put
OrderedLocusNames=TDE0171; ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSM 9941."
Submitted
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
STRAIN-ATCC 35405 / DSM 14222;
PubMede-15064399; DOI=10.1073/pnas.0307639101;
Seshadri R., Myers G.S.A., Tettelin H., Eisen
                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00133; tRNA-synt 1; 1.

PRINTS; PR00946; TRNASYNTHAL.

TIGRA0422; vals; 1.

PROSITE; PS00178; AA_TRNA_LIGASE I; 1.

PROSITE; PS00178; AA_TRNA_LIGASE I; 1.

PROSITE; PS00178; AM_TRNA_LIGASE; Ligase;

PROSITE; PS00178; AM_TRNA_SYNTHEtase; Ligase;
                                                                                        Bacteria; Spirochaetes;
                                                                                                    Treponema denticola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002300; tRNA-synt_1a.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002303; tRNA-synt_val.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Hammon N., Israni S., Pitluck S., Richardson P.; Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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xylanophilus DSM 9941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOE Joint
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0005524; F:ATP binding; IEA.
GO:0016874; F:ligase activity; IEA.
GO:0000166; F:nuclectide binding; IEA.
GO:0004832; F:valine-TRNA ligase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0006412; P:protein biosynthesis; IEA. GO:0006438; P:valyl-tRNA aminoacylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary data.
CATALYTIC ACTIVITY: ATP + L-valine + tRNA(Val)
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                                                                                                                                                                                                                                                                               607
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BUNIT: Monomer (F
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                                                                                                                                                                                                                                                                                                                                                                                                           biosynthesis.
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                                                                                                                                                                                                                                                                                                                                     Conservative
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Genome Institute (JGI-PGF);
Genome Institute (JGI-PGF);
                                                                                                                                                                          integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                            97415 MW;
                                            [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                 89.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
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                                                                                                                putative.
ORFNames=TDE_0171;
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  Eisen
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RESULT 21
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13-SEP-2005,
07-FEB-2006,
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                                 Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Hammon N., Israni S., Pitluck S., Richardson P.; Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                             "Sequencing of the draft vietnamiensis G4.";
                                                                                                                                                                                                                                                          Copeland A., Lucas S., Lapidus A., Barry K., Hammon N., Israni S., Pitluck S., Richardson "Sequencing of the draft genome and assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q4B833_BURVI
Q4B833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with other spirochete genomes."; Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
                                                           US DOE Joint Genome Institute (JGI-PGF); Copeland A., Lucas S., Lapidus A., Barry K.,
                                                                                                                             Submitted
                                                                                                                                                                               STRAIN=G4;
US DOE Joint Genome Institute
                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                 US DOE Joint
                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Betaproteobacteria;
Burkholderiaceae; Burkholderia; Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                           Burkholderia vietnamiensis G4.
                                                                                                                                                                                                                                                                                                                                                                                                       ORFNames=Bcep1808DRAFT_0224;
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GO; GO:0016887; F:ATPase activity;
InterPro; IPR003439; ABC_transp_118
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GenomeReviews; AE017226_GR; TDE0171.
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                                                                                                                                                      "Annotation
                                                                                                                                                                    Larimer
                                                                                                                                                                                                          NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=269482;
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         CAUTION: The sequence shown here is derived EMBL/GenBank/DDBJ whole genome shotgun (WGS)
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                                                          Lucas S.,
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                                                                                                                                                     assembly of Burkholderia vietnamiensis
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3.7e+02;
0;
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Attribution-NoDerivs License
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P.;
of Burk
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                                                                                                                              databases
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                        from an
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          entry which
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RESULT 23
Q2UDO8 ASPOR
ID QZUDO8;
DT Q4-JAN-2006, i
DT 24-JAN-2006, s
DT 07-MAR-2006, s
DT 07-MAR-2005, s
DT 07-MAR-2005, s
DT 07-MAR-2005, s
DT 07-MAR-2005
GN ORFNames=A0090
OS Aspergillus or
OC Eukaryota; Fun
OC Eukaryota; Fun
OC Eurotiales; Tx
OX NCBI TaxID=506
RN [1]
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RX PubMed=1637201
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Best Local S
Matches 6
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GO; GO:00
Pyruvate.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu B., Zhao B., Wang X.Y., Xu Y.Y., Liu Y.Q., Song L., Ye Sheng H., Gao Y., Zhang C.L., Wei Y.J., Zhang J., Song L., Zhao Z.W., Ding J.F., Liu L.S., Gao R.L., Wu Q.Y., Qiang B. Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O5QTR8;
04-JAN-2005, integrated into U
04-JAN-2005, sequence version
04-JAN-2006, serve version 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                              24-JAN-2006, integrated into UniProtKB/TrEMBL. 24-JAN-2006, sequence version 1. 07-MAR-2006, entry version 3. Hydrolases of the alpha/beta superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
NUCLEOTIDE SEQUENCE.
STRAIN=RIB 40;
PubMed=16372010; DOI=10.1038/nature04300;
                                                                       Eukaryota; Fungi; Ascomycota
Eurotiales; Trichocomaceae;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
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                                                                                                                  ORFNames=A0090012000367;
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                                                                                                     Aspergillus oryzae
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les 6; Conserv
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GO:0016491; F:oxidoreductase activity; IEA.
GO:0006118; P:electron transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                      AF109190; AAQ13500.1; -; mRNA.
NCE 44 AA; 5210 MW; 90754272D3B001A4
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                                                                                         Ascomycota;
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85.7%;
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                                                                        mitosporic Trichocomaceae; Aspergillus.
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Pred. No.
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Rikusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,

Ah Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,

Balagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,

Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,

Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,

Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,

Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,

Rato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,

Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,

Na Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,

Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,

Na Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,

Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,

Kuhara S., Ogasawara N., Kikuchi H.;

Wature 438:1157-1161(2005).
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Best Local Similarity
                                                                              PubMed=14702039, DOI=10.1038/ng1285;
PubMed=14702039, DOI=10.1038/ng1285;
Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Tshida S.,
Ono Y., Takiguchi S., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
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LHUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRG4 HUMAN STANDARD; PRT; 1404 AA.

929254; Q6DNC4; Q6DNC5; Q6ZNZ5; Q9BX49;

06-DEC-2005, integrated into UniProtKB/Swiss-Prot.

06-DEC-2005, sequence version 2.

07-MAR-2006, entry version 38.

Proteoglycan-4 precursor (Lubricin) (Megakaryocyte stimulating factor)

(Superficial zone proteoglycan) [Contains: Proteoglycan-4 C-terminal
Kanehori K., 7
Togiya S., Kon
Musashino K.,
                                                                       Tanai H., Kimar
Omo Y., Takiguchi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NÜCLEOTIDE SEQUENCE [MRNA] (ISOFORM A), AND VARIANT TRP-180 Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Lee Kelleher K., Giannotti J., Caletti J., Fitzgerald M., Kriz Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gebhatta S., Kriz R., Hewick R., Clark S.C.; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=PRG4; Synonyms=MSF, SZP;
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Euarchont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Synovial cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM E)
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GO:0016787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168
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   kiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.
1., Takahashi-Pujii A., Hara H., Tanaea T.-O., Nomura Y.,
Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33626 MW;
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85.7%;
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Pred. No. 1.7e+02;
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n C.R., Gesne
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VA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Momiyama H., Satoh N., Takamai S., Terashima Y., Suzuki O., A Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., A Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., A Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Fujiwara T., A Yamazaki M., Watanabe K., Kumagai A., Tahigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., A Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sagaki M., A Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., A Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., A Makai K., Yada T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., "Complete sequencing and characterization of 21,243 full-length human T., "Complete sequencing and characterization of 21,243 full-length human T., "Complete sequencing and characterization of 21,243 full-length human T., "Complete sequencing and characterization of 21,243 full-length human T., "Complete sequencing and characterization of 21,243 full-length human T., "Complete sequencing and characterization of 21,243 full-length human T., "Complete Sequencing and Characterization of 21,243 full-length human T., "Complete Sequencing and Characterization of 21,243 full-length human T., "Complete Sequencing and Characterization of 21,243 full-length human T., "Complete Sequencing and Characterization of 21,243 full-length human T., "Complete Sequencing and Characterization of 21,243 full-length human T., "Complete Sequencing and Characterization of 21,243 full-length human T., "Complete Sequencing and Characterization of 21,243 full-length human T., "Complete Sequencing and Characterization of 21,243 full-length human T., "Complete Sequencing and Characterization of 21,243 full-length human T., "Co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uones A.R., Hughes C.E., Flannery C.R., Caterson B.;
"Cloning and production of recombinant PRG4/cartilage superficial zone proteoglycan (SZP) N- and C-terminal domains.";
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ datahases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=14976050; DOI=10.1182/blood-2003-06-1825; Liu Y.J., Lu S.H., Xu B., Yang R.C., Ren Q., Liu Yan F.Y., Han Z.B., Han Z.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flannery C.R., Hughes C.E., Schumacher B.L., Tudor D., Aydelotte M. Kuettner K.E., Caterson B.;
"Articular cartilage superficial zone protein (SZP) is homologous to megakaryocyte stimulating factor precursor and is a multifunctional proteoglycan with potential growth-promoting, cytoprotective, and lubricating properties in cartilage metabolism.", Biochem. Biophys. Res. Commun. 254:535-541(1999).
GLYCOSYLATION.
MEDLINE=94241694;
Schumacher B.L., /
                                                                                                                                      "A comparison of vitronectin and (In) Preissner K.T., Rosenblatt Mosher D.F. (eds.);
                                                                                                                                                                                                      Merberg D.M., Fitz L.J., Temple P., Giannotti J., Murtha Fitzgerald M., Scaltreto H., Kelleher K., Preissner K., Jacobs K., Turner K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA] OF 39-5
IDENTIFICATION OF ISOFORM C.
MEDLINE-99120896; PubMed-9920774;
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                                                                                            Science
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                                                                                       of vitronectins
Publishers B.V.,
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    Block
    PubMed=8185311;
Block J.A., Schmi
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                                                                                                                 their
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                                                                                                                                                           megakaryocyte stimulating S., Kost C., Wegerhoff J.,
    DOI=10.1006/abbi.1994.1219;
id T.M., Aydelotte M.B.,
                                                                                            receptors,
m (1993).
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i J., Fitzgerald M., Kı
Bean K., Norton C.R.,
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                                                                                                                                                                                                                                                                                                                                                                    has megakaryocyte
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  Aydelotte
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riz M.-J.,
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Marcelino u.,
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Robbins C., Sood R., Makalowska I., Baxevanis A., Johnstone
Laxer R.M., Zemel L., Kim C.A., Herd J.K., Ihle J., Williams
Johnson M., Raman V., Alonso L.G., Brunoni D., Gerstein A.,
Papadopoulos N., Bahabri S.A., Trent J.M., Warman M.L.;
"CACP, encoding a secreted proteoglycan, is mutated in campt
arthropathy-coxa vara-pericarditis syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [13]
CARBOHYDRATE-LINKAGE SITE ASN-1159.
PubMed=16335952; DOI=10.1021/pr0502065;
PubMed=16335952; DOI=10.1021/pr0502065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jay G.D., Britt D.E., Cha C.-J.;
"Lubricin is a product of megakaryocyte stimulating expression by human synovial fibroblasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A novel proteoglycan superficial zone of an Arch. Biochem. Biophys
                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hydrazide chemistry, and mass spectrometry.";
J. Proteome Res. 4:2070-2080(2005).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=10743795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (proteoglycan 4) genes
Cytogenet. Cell Genet.
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"Isolation, characterization and mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10545950; DOI=10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rheumatol.
                                                                                             TISSUE SPECIFICITY: Highly expressed in synovial tissue, cartilage and liver, and weakly in heart and lung. Isoform B is expressed in kidney, lung, liver, heart and brain. Isoform C and isoform D are widely expressed.

PTM: N-glycosylated.

PTM: 0-glycosylated. contains glycosaminoglycan chondroitin
for protein cleavage (By similarity). DISEASE: Defects in PRG4 are the cause of camptodactyly-arthropathy-coxa vara-pericarditis syndrome (CACP) [MIM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       surface.
FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           articulating joints. Prevents protein deposition onto cartilage from synovial fluid, control adhesion-dependent synovial growth and inhibit the adhesion of synovial cells to the cartilage
                                                         sulfate and keratan sulfate.
PTM: The disulfide bond between Cys.1146 and
                                                                                                                                                                                                                             Name=F; Synonyms=Hemangiopoietin, HAPC
IsoId=Q92954-6; Sequence=VSP_016469;
                                                                                                                                                                                                                                                                                                                                                                                               Name=C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Secreted ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primitive cells
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    genes."

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articular cartilage.";
hys. 311:144-152(1994).
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[MIM:208250];

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Best Local
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SEQUENCE
ORFNames=GSTENG00022129001;
Tetraodon nigroviridis (Green
Eukaryota; Metazoa; Chordata;
                                                                                                 19-JUL-2005, integrated into UniProtK
19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 3.
Chromosome 7 SCAF14003, whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]. COCCELAND A., Lucas S., Lapidus A., Barry K., Detrer J.C., G. Copeland A., Israni S., Pitluck S., Goltsman E., Martinez M., Schmutz J., Larimer F., Land M., Lykidis A., Richardson P.; "Complete sequence of chromosome 2 of Ralstonia eutropha JMI Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ralstonia eutropha (strain JMP134) (Alcaligenes eutrophus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q46TT1_RALEJ
Q46TT1;
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                                                                                                                                                                                                                                                   Q4S8Z0_TETNG
Q4S8Z0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OrderedLocusNames=Reut_B4097;
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13-SEP-2005,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burkholderiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-2006,
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TETNG
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RALEJ
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MISCELLANEOUS: Different forms of various molecular weight have miscellaneous are possibly due to different levels of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      been observed. Such forms are possibly due to diffe glycosylation and protein cleavage (By similarity). SIMILARITY: Contains 2 hemopexin-like domains. SIMILARITY: Contains 2 SMB (somatomedin B) domains.
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ilarity 71.4%;
Conservative
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Pred. No. 8.4e
0; Mismatches
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Q43Q96_SOLUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                 13-SEP-2005, 13-SEP-2005, 1
                                                                                                                                US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K.,
Hammon N., Israni S., Pitluck S., Richardson
"Sequencing of the draft genome and assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
Genoscope; Whitehead Institute Centre for Genome Researc
Genoscope; Whitehead Institute Centre for Genome Researc
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w
                                                                                                                                                                                                                                                                                                                  Transport-associated ORFNames=AcidDRAFT_11
                                                                                                                                                                                                                                                                                                                                                                                                  Q43Q96_SOLUS
Q43Q96;
 US DOE Joint Genome Institute (JGI-ORNL);
Larimer F., Land M.;
"Annotation of the draft genome assembly
                                                                                                                                                                                                NUCLEOTIDE SEQUENCE. STRAIN=Ellin6076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                   STRAIN=Ellin6076;
                                                                                                                  "Sequencing of the Ellin6076.";
                                                                                                                                                                                                                                                                                 Bacteria; Acidobacteria;
                                                                                                                                                                                                                                                                                                 Solibacter usitatus Ellin6076
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Tetradontoidea; Tetraodontidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
"Annotation
                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                               NCBI_TaxID=234267;
                                                                                                                                                                                                                                                                   Solibacteraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.
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                                                                                                  (JUN-2005)
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                                                                                                                                                                                                                                                                                                                                                                                    integrated into UniProtKB/TrEMBL.
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                                                                                                                                                                                                                                                                   Solibacter.
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71.4%;
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   genome assembly of Solibacter usitatus.";
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8D07018118B6F483 CRC64;
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Tetraodon.
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of Solibacter
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WMLSAYA 157

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QPWXJ3 PORGI
ID Q9WXJ3;
AC Q9WXJ3
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Q9WXJ3;
01-NOV-1999,
01-NOV-1999,
07-FEB-2006,
                                                                                                                                                                                  PROSITE;
PROSITE;
SEQUENCE
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SIGNAL
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                                                                                                                                                                                                                                                                                                                      Pfam; PF00210; Ferritin; 1
                                                                                                                                                                                                                                                                                                                                 GO; GO:0008199; F:ferric iron binding; IEA.
GO; GO:00068199; P:iron ion homeostasis; IEA.
GO; GO:0006950; P:response to stress; IEA.
InterPro; IPR002177; DPS DNA bd.
InterPro; IPR008331; Ferritin_Dps.
InterPro; IPR012347; Ferritin_rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB025779; BAA76886.1; -; Genomic_DNA. HSSP; Q8RPQ1; 1JIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Purification, gene cloning, gene expression, and the obligate anaerobe Porphyromonas gingivalis."; Infect. Immun. 71:1170-1178(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 33277;
MEDLINE=22483669; PubMed=12595429;
DOI=10.1128/IAI.71.3.1170-1178.2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=837;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=dps;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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PROSITE; PS50914; BON; 1.
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                                                                                                                                                                                  3; PR01346; HELNAPAPROT.
1; PD149803; DPS; 1.
18; PS00818; DPS 1; 1.
18; PS00819; DPS 2; 1.
10E 159 AA; 17793 MW;
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                                                                               Similarity 5; Conserv
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                                                                                                        Score 32;
Pred. No.
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: A7290632DFF510E4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    see http://www.uniprot.org/terms
                                                                                                                                   DB 2;
                                                                                                           .5e+02;
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                                                                                                                                                                                        CRC64;
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RESULT 29
Q7MXS1_PORGI
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Q7MXS1;
15-DEC-2003,
15-DEC-2003,
07-FEB-2006,
                                                                                                        01-JUN-2003,
01-JUN-2003,
07-FEB-2006,
             Name=0J9990 A01.131; Synonyms=0J1449 C
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOI=10.1128/JB.165.18.5591-5601.2003;
Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fout Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J., Dewhirst F.E., Fraser C.M.;
"Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";
J. Bacteriol. 185:5591-5601(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD149803; DPS; 1.
PROSITE; PS00818; DPS_2; 1.
PROSITE; PS00819; DPS_2; 1.
Complete proteome.
SEQUENCE 159 AA; 17865 M
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TIGR; PG0090; -
                                                                       Hypothetical political of OJ1449_C01.14
                                                                                                                                                              Q84S36_ORYSA
Q84S36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BioCyc; PGIN242619:PG0090-MONOMER;
GO; GO:0008199; F:ferric iron bind
GO; GO:0006879; P:iron ion homeost
GO; GO:0006950; P:response to stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Bacteria; Bacteroidetes; Bacteroidetes
Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=PG0090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00210; Ferritin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22829867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=W83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dps family protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR012347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002177; DPS
InterPro; IPR008331; Feri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=837;
                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE015924;
                                                                                                                                                                                                                                                                                                            μ.
                                                                                                                                                                                                                                                                                                                                              Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PR01346; HELNAPAPROT.
                                                                                                                                                                                                                                                                                                            WMLSAFS 7
                                                                                                                                                                                                                                                                          WMLSAYA 157
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence version entry version 14.
                                                                                                           entry version 9.
                                                                                      protein OJ9990
                                                                                                                                           integrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             integrated into
 Magnoliophyta;
                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ65337.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=12949112;
                                                                                                                                                                                                                                                                                                                                                                                                                        17865 MW;
                                                                                                                                                                                                                                                                                                                                                               84.2%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ferritin_rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPS_DNA_bd.
Ferritin_Dps.
                                                    Synonyms=0J1449_C01.14;
                                                                                                                                             into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iron binding; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORFNames=PG_0090;
(Bacteroides gingivalis)
tr.rai-gruup,
Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae; BEP clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homeostasis;
                                                                                        A01.131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                 Score 32; I
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                      60889B904D331AC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                      (Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159
                                                                                                                                                                                 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IEA.
                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                               .5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                  Length 159;
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gwinn M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fouts D.E.,
                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                Gaps
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RASILLT 31
Q4SFB2 TETNG
ID Q4SFB2 T
DT 19-JUL-2
DT 19-
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=15496914; DOI=10.1038/nature03025;
Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Biemont C., Skalli Z., Cattollco L., Poulain J., De Berardinis V.,
Cruaud C., Duprat S., Brottier P., Couranceau J.-P., Gouzy J.,
Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.
Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tetraodon nigroviridis (Green puffer).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q4SFB2;
19-JUL-2005, integrated into UniProtXB/TrEMBL.
19-JUL-2005, sequence version 1.
07-FEB-2006, entry version 3.
Chromosome 6 SCAF14605, whole genome shotgun sequence.
ORFNames=GSTENG00019173001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki T., Matsumoto T., Katayose "Oryza sativa nipponbare(GA3) genc clone:OJ1449_CO1.";
                             NUCLEOTIDE SEQUENCE.
Genoscope; whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry whi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical SEQUENCE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sasaki T., Matsumoto T., Katayose Y.; "Oryza sativa nipponbare(GA3) genomic DNA, clone:OJ9990_A01.";
                                                                                                                                                                                                                                                       Laudet V., Schachter V., Quetier F., Saurin W., Robinson-Rechavi M., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.";

Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q4SFB2_TETNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (\widetilde{AUG}-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ehrhartoideae; Oryzeae; Oryza
NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gramene; Q84S36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP005847;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WMLSAFS 7
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167 AA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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        data
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71.4%;
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Pred. No. 1.6e+02;
2; Mismatches 0
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genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 8,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
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Best Local
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Best Local
                                                                                                                                                                      InterPro; IPR004153; CXCXC_repeat.
InterPro; IPR00853; TMEM9.
PANTHER, PTHR13064; TMEM9; 1.
Pfam; PF03128; CXCXC; 1.
Pfam; PF05434; TMEM9; 1.
Hypothetical protein; Membrane; Tran
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01-AUG-1998,
07-FEB-2006,
                                                                                                     TRANSMEM
TRANSMEM
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [GENOMIC DNA].

Riboldi Tunnicliffe G.R., Platzer M., Nyakatura G., Elga
Riboldi Tunnicliffe G.R., Platzer M., Nyakatura G., Elga
Riboldi Tunnicliffe G.R., Platzer M., Nyakatura G., Elga
Barenner S., Rosenthal A.;

"Analysis of the genomic loci of Fugu rubripes homologs
disease genes L1CAM, G6PD and P55.";

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FBB-2006, entry version 28.
Putative protein 2 (PUT2) (Fragment).
Putative protein 2 (PUT2) (Fragment).
Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Meoterygii; Teleostei; Euteleostei; Neoteleostei;
Acatinopterygii, Reanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUT2_FUGRU
073698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/topistributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                   GO; GO:0005770; C:late endosome; GO; GO:0005764; C:lysosome; ISS.
                                                                                                                                                                                                                                                                                             Ensembl; SINFRUG00000152263; Fugu
                                                                                                                                                                                                                                                                                                           PIR; T30536; T30536.
                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the TMEM9 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=31033;
                                                                                                                                                                                                                                                                                                                                                                                                          Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAE01014605; CAG00670.1; -; Genomic_DNA.
NCE 182 AA; 20009 MW; 0869B43C89CB7475
                                                                                                                                                                                                                                                                                                                         AF026198; AAC15584.1; -;
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 9
                                                  Similarity 5; Conserv
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                          WMLSAFS
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 WMLAAFA 15
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187
187
                                                     Conservative
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121
187
21460
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Pred. No. 1.7e
0; Mismatches
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                                                               Pred.
                                                                            Score 32;
                                                                                                                              /FTId=PRO 0000221039 Potential.
                                                                                                                                                                      e; Transmembrane.
Putative protein
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                                                                                                      51DD101FE4666D3B CRC64;
                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
1.7e+02;
                                                                             DB 1;
                                                               7e+02;
                                                                                                                                                                        N
                                                     0
                                                                          Length 187;
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RESULT 33 Q6CXD3\_KLULA

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Q6ZRV1 HUN-
ID Q6ZRV2
PO C5-U
DT 05-U
DT 05-U
DT 05-U
DT 05-U
DT 05-U
DT 21-FE
DE CDNA
DB 1acte
DC Homo
OC Eukar
OC Mamma
OC Mamma
OC Momo
OC Micho
OC Mich

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X PubMed=15229592; DOI=10.1038/nature02579;

X Dujon B., Sherman D., Fischer G., Durrens P., Cassaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,

A Despons L., Fabre E., Jauniaux N., Joyet P., Kachouri R.,

A Mantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

A Micaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

A Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

A Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

A Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

A Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,

Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,

Mincker P., Souciet J.-L.;

"Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete
SEQUENCE
Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y. Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
                                                                                                                                                                                                                                                                                                                                                                05-UUL-2004, integrated into UniProtKB/TrEMBL.
05-UUL-2004, sequence version 1.
21-FBB-2006, entry version 13.
CDNA FLJ46073 fis, clone TEST12001364, highly lactate dehydrogenase A -like (LDHL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Kluyveromyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-2006, entry version 12.
Similar to sp|P38869 Saccharomy
OrderedLocusNames=KLLAOA09295g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q6ZRV1_HUMAN
Q6ZRV1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF04148; DUF396; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; PANTHER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 430:35-44(2004).
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Q6CXD3;
                                                                                                                                             TISSUE=Testis;
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                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                              _TaxID=9606;
                                                                                                                                                                                                                                                                                                                                            sapiens (Human).
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5; Conserv
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226 AA;
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Euarchontoglires; Primates;
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Pred. No. 2.1e+02;
2; Mismatches 0;
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rimates; Catarrhini; Homin
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RESULT 35

### P72049 MYCTU PRELIMINARY; PRT; 280 AA.

### P72049 MYCTU PRELIMINARY; PRT; 280 AA.

#### AC P72049; Q7D4V5;

### Q7D4V5;

### Q7-FEB-1997, integrated into UniProtKB/TrEMBL.

### DT 01-FEB-1997, sequence version 1.

### DT 07-FEB-2006, entry version 31.

### DE PROBABLE O-ANTIGEN/LIPOPOLYSACCHARIDE TRANSPORT INTEGRAL MEMBRANE DE PROTEIN ABC TRANSPORTER RFBD (O-antigen export system, permease DE PROTEIN ABC TRANSPORTER RFBD (O-antigen export system, permease DE PROTEIN ABC TRANSPORTER RFBD (O-antigen export system, permease DE PROTEIN ABC TRANSPORTER RFBD (O-antigen export system, permease DE PROTEIN ABC TRANSPORTER RFBD (O-antigen export system, permease DE PROTEIN ABC TRANSPORTER RFBD (O-antigen export system, permease DE PROTEIN ABC TRANSPORTER RFBD (O-antigen export system, permease DE PROTEIN ABC TRANSPORTER RFBD (O-antigen export system, permease DE PROTEIN ABC TRANSPORTER RFBD (O-antigen export system)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001557; L_LDH_MDH.
InterPro; IPR011304; L_LDH_MAD.
InterPro; IPR011236; lact_mal_DH.
InterPro; IPR000205; NAD_BS.
InterPro; IPR000594; Thif NAD_FAD_k
PANTHER; PTHR11540; ldh; I.
Pfam; PF02866; Ldh 1 C; 1.
Pfam; PF00056; Ldh 1 N; 1.
NUCLEOTIDE SEQUENCE
STRAIN=CDC 1551 / Oshkosh;
STRAIN=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
DOI=10.1128/JB.184.19.5479-5490.2002;
DOI=10.1128/JB.184.19.5479-5490.2002;
                                                                                                                                                                                                                                                                                                                Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M., Harris D.E., Gordon S.V., Eigimeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares R., Rogers J., Taylor K., Whitehead S., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; FROSITE;
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                                                                                                                                                                                                                                     "Deciphering the biology of Mycobacterium complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0004459; F:L-lactate dehydrogenase activity; GO; GO:0006491; F:oxidoreductase activity; IEA. GO; GO:0006096; P:glycolysis; IEA. GO; GO:0006100; P:tricarboxylic acid cycle intermed:
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STRAIN=H37Rv;
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; PS00064; L_LDH; UNKNOWN 1.
E 243 AA; 26419 MW; 98D3B92406208F25 CRC64;
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Complete SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TubercuList; Rv3783; -. GO; GO:0016020; C:membrane; IEA. GO; GO:0015524; F:ATP binding; IEA. GO; GO:0005524; F:ATP binding; IEA. GO; GO:0042626; F:ATPase activity, coupled GO; GO:006810; P:transport; IEA. InterPro; IPR000412; ABC_2. Pfam; PF01061; ABC2 membrane; 1. Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE STRAIN=AF2122/97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
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07-FEB-2006, entry version 11.
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Distributed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
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erPro; IPR000412; ABC_2.
                                                                                                                            .; BXZ48347; CAD95998.1; -; Genomic_DNA.
GO:0016020; C:membrane; IEA.
GO:0005524; F:ATPase activity, coupled.
GO:0042626; F:ATPase activity,
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                                                                                                                                                                                                                                                                by the UniProt Consortium, see http://www.uniprot.org/terms under the Creative Commons Attribution-NoDerivs License
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07-FEB-2006, entry version 22.
Mas-related G-protein coupled receptor member G (breakpoint transcript 2 protein).
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PRINTS; PRO0237; G PROTEIN RECEP_F1_2; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; FALSE_NEG.
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Distributed under the Creative Commons Attribution NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The BWS region contains an evolutionary breakpoint reg. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Engemann S., Stroedicke M., Meguro M., Oshimura M., Walter J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21435808; PubMed=11551509; DOI Dong X., Han S.-K., Zylka M.J., Simon "A diverse family of GPCRs expressed i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Euarchontogi
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Mrgprg; Synonyms=Ebrt2,
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRGRG_MOUSE
Q91ZB5; Q711N2;
                                                                                                                                                                                                                                                                                                                                                                                                                               Ensembl; ENSMUSG00000050276; Mus m
MGI; MGI:3033145; Mrgprg.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I- FUNCTION: Orphan receptor. May regulate nociceptor function and/or development, including the sensation or modulation of pain.
-I- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
-I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                          Transmembrane.
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00001; 7tm
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AJ313465; CAC86130.1; -; mRNA.
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5; Conserv
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mon M.I., Anderson D.J.;
ed in specific subsets of
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                                                                                                                                                                                                                                                                                                                     Receptor; Transducer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  see http://www.uniprot.org/terms
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AS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
AS Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
AA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
AA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
AA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
AA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
AA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
AA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
AB Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
AB Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
AB Asha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
AR Asha S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
AR Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
AN ARIAN J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
AN Ahiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
AR AN Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
AR AN Hallon D.K., Mitter S., Garcia B.D., Dickson M.C.,
AR AN Hallon D.K., Krzywinski M.I., Skalska U., Smailus D.E.,
AR Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
T. Tock Maria And Schien J.E., Jones S.J.M., Marra M.A.;
Thand mouse cDNA sequences.";
A Dollage S. J.M., Marra M.A.;
Thand mouse cDNA sequences.";
A Dollage S. J.M., Marra M.A.;

A Dollage S. J. M. S. S. J.M., Marra M.A.;
Thand mouse cDNA sequences.";
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CONFLICT
EMBL; BC100302; AAI00303.1; -; mRNA.
MGI; MGI:3033145; Mrgprg.
GG; GO:0016021; C:integral to membrane; IEA.
GG; GO:0016020; C:membrane; IEA.
GG; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity;
GO; GO:0007186; P:G-protein coupled receptor proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                              Copyrighted by the UniProt
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mitted (AUG-2005) to the
SUBCELLULAR LOCATION:
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embrane; multi-pass membrane
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6 (Potential).
Extracellular (Potential)
7 (Potential).
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f
                                                                                                                                                                                                                                 see http://www.uniprot.org/terms
Attribution-NoDerivs License
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        protein signalin.
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RESULT 40
Q2TWR7_9DIPT
ID Q2TWR7;
ID Q2TWR7;
AC Q2TWR7;
DT 24-JAN-2006, s
DT 24-JAN-2006, s
DT 07-MAR-2006, s
DT 07-MAR-2016, s
DT 07-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 39
Q3M9S1_ANA
ID Q3M9S
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Matches
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Best Local
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Q3M9S1 ANAVT
Q3M9S1;
25-OCT-2005,
25-OCT-2006,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US DOE Joint Genome Institute;
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C.,
Hammon N., Israni S., Pitluck S., Saunders E.H., Schmutz
Larimer F., Land M., Kyrpides N., Mavrommatis K., Richard
"Complete sequence of Anabaena variabilis ATCC 29413.";
Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                              07-MAR-2006, entry version NADH dehydrogenase subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
ORFNames=Ava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-protein coupled receptor; Membrane; Receptor; Transducer;
                                                                                   Neoptera; Endopterygota; Di
Ephydroidea; Drosophilidae;
                                                                                                                                                        Mitochondrion.
                                                                                                                                                                            Drosophila unimaculata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; SIGNAL 1 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; CP000117; ABA22265.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=ATCC 29413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anabaena varīabilis (strain ATCC 29413).
Bacteria; Cyanobacteria; Nostocales; Nos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
  NUCLEOTIDE SEQUENCE. Wang B.-C., Park J.,
                                                             NCBI_TaxID=311483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=240292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0007165; P:signal transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                      17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WMLSAFS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WLLAAFS 100
                                                                                                                                                                                                                                                                                                                                                                                                                      WLLSSFS
                                                                                                                               Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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2652;
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                                                                                                                                                                                                                                                                integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                            sequence version
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                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                      23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37291 MW;
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71.4%;
      Watabe
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    3.
    2 (Fragment).

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      H.-A.,
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; 1F1E00BAF83097F3 CRC64;
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 2;
Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                          Hexapoda; Insecta; Pterygota;
a; Brachycera; Muscomorpha;
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      Gao
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      J.-J.,
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      Aotsuka
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      Τ.,
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      Chen H.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.
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RESULTIVE PROPERTY OF THE PROP
RESULT 42
Q2TNS6_9DIPT
ID Q2TNS6_9DIPT
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Best Local
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IS2_9DIPT
QZTNS2_9DIPT
Q2TNS2;
                                                                                                                                                                                                                                                                                                                              NON TER
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24-JAN-2006,
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-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol-
-!- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner m multi-pass membrane protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion; NAD; Ox:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/tuDistributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                          EMBL; AY750079; AAX52010.1; -; Genomic_DNA.
EMBL; AY750074; AAX52005.1; -; Genomic_DNA.
GO; GO:0005739; C:mitochondrion; IEA.
Mitochondrion; Ubiquinone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ub: -!- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JAN-2006, sequence version 1.
07-MAR-2006, entry version 3.
NADH dehydrogenase subunit 2 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Phylogenetic analysis of the Drosophila robusta and melanica groups based on mitochondrial and nuclear DNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
Wang B.-C., Park J., Watabe H.-A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila medioconstricta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multi-pass membrane protein (By similarity).
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                                                                                                                                      WMLSALS 191
                                                                                                                                                                                     WMLSAFS 7
                                                                                                                                                                                                                                                                                                                              341
341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 AA;
                                                                                                                                                                                                                                    Conservative
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               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                 39472 MW;
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85.7%;
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Pred. No. 3.2e+02;
D; Mismatches 1
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               PRT;
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                                                                                                                                                                                                                                                                                                                                 FCA6B7F94E90A733 CRC64;
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               341
                                                                                                                                                                                                                                                                                DB 2;
               B
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                                                                                                                                                                                                                                                                                Length 341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            + ubiquinol.
|rial inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ubiquinol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                    Gaps
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RESULT
Q2TNT2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                          24-JAN-2006,
24-JAN-2006,
07-MAR-2006,
                                                                                                                                                                                                                                                                                                                                             LT 43
T2 9DIPT
Q2TNT2 9DIPT
Q2TNT2;
                                                                                                    NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   groups based on mitochondrial and nuclear DNA sequ
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ data
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JAN-2006, integrated into UniProtKB/TrEMBL.
24-JAN-2006, sequence version 1.
07-MAR-2006, entry version 3.
NADH dehydrogenase subunit 2 (Fragment).
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neoptera; Endopterygota; Di
Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila medioconstricta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q2TNS6;
                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                               07-MAR-2006, entry version 3. NADH dehydrogenase subunit 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AY750075; AAX52006.1; -; GGO; GO:0005739; C:mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=311480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
          Mitochondrion; NAD; Oxidoreductase; Ubiquinone
                                           EMBL; AY750069; AAX52000.1; -; Genomic_DNA
                                                                                                                                                                          Wang B.-C.,
Zhang Y.-P.;
                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                          Mitochondrion
                                                                                                                                                                                                                                                                                    Drosophila tsigana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion; Ubiquinone.

    -!- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang Y.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
Wang B.-C., Park J.,
 SEQUENCE
                                                                                                                                                                 "Phylogenetic analysis of the Drosophila robusta and melanica
                                                                                                                                                                                                                       NCBI_TaxID=65966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Phylogenetic analysis of the Drosophila robusta and
                                 GO:0005739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multi-pass membrane protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                      185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              WMLSAFS
                                                                                                                                                                                                                                                                                                                                                                                                                      WMLSALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 AA;
                                                                                                                                                                                       Park J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                      sequence version 1.
                                                                                                                                                                                                                                                                                                                                   integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                   C:mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                       191
                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39515
  39589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.2%;
85.7%;
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                                                                                                                                                                                      Watabe H.-A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
 X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 2;
Pred. No. 3.2e+02;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                  (Fragment).
                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72DF506731F85349 CRC64;
 A9B3CC084A3B5B95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEA.
                                    IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachycera; Muscomorpha;
                                                                                                                                                                                      Gao J.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gao J.-J., Aotsuka
                                                                                                                                                                                                                                                                                                                                                           341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences.";
                                                                                                                                                                                       Aotsuka T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                             Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ubiquinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          melanica
                                                                                                                               ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen
                                                                                                                                                                                      Chen H.-W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane;
                                                                                                                    membrane;
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RESULT 45
Q2TNT5_9DIPT
ID Q2TNT5;
DT Q2TNT5;
DT 24-7AN-2006, s
DT 07-MAR-2006, s
DT 07-MAR-2016 e
DE NADH dehydroge
OS Drosophila mor
OG Mitochondrion.
OC Eukaryota; Mete
OC Neoptera; Ende
OC Neoptera; Ende
OC Ephydroidea; D
OX NCBI_TaxID=107
RN [1]
RP NUCLEOTIDE SEC
RA Wang B.-C., Pa
RA Zhang Y.-P.;
RT "Phylogenetic
RT "Phylogenetic
RT groups based o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 44

QZTWT3 9DIPT
ID QZTWT3;
DT 24-JAN-2
DT 24-JAN-2
DT 07-MAR-2
DE NADH deh
OS Drosophi
OG Eukaryot
OC Neoptera
OC Neop
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JAN-2006,
24-JAN-2006,
07-MAR-2006,
NUCLEOTIDE SEQUENCE.
Wang B.-C., Park J., Watabe H.
Zhang Y.-P.;
"Phylogenetic analysis of the
groups based on mitochondrial
                                                                                                                                                                                                                                                                                                                       24-JAN-2006, integrated into Uni
24-JAN-2006, sequence version 1.
07-MAR-2006, entry version 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Phylogenetic analysis of the Drosophila robusta and melanica s
groups based on mitochondrial and nuclear DNA sequences.";
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner me
multi-pass membrane protein (By similarity).
                                                                                                                                                                            Neoptera; Endopterygota; Dip
Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                     Drosophila moriwakii.
                                                                                                                                                                                                                                                                                                        NADH dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY750068; AAX51999.1; -; Genomic_DNA. GO; GO:0005739; C:mitochondrion; IEA. Mitochondrion; NAD; Oxidoreductase; Ubiquinone. NON_TER 341 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang B.-C.,
Zhang Y.-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
Wang B.-C., Park J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ephydroidea; Drosc
NCBI_TaxID=311477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila paramelanica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NADH dehydrogenase subunit 2 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QZTNT3_9DIPT
QZTNT3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WMLSALS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WMLSAMS 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry version 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                          subunit 2 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39575 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.2%;
85.7%;
                                                                         Watabe H.-A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Watabe H.-A.,
                                                                                                                                                                                                       Diptera; Brachycera;
                                                                                                                                                                               Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32; DB Pred. No. 3.2e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                      UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
     Drosophila robusta and melanica species and nuclear DNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4A1428DBA3BE5EBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gao J.-J., Aotsuka
                                                                         Gao J.-J., Aotsuka T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2e+02;
  DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                         Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inner membrane;
                                                                              Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 47
Q2TNT7_DROMX
ID Q2TNT7,
AC Q2TNT7,
DT 24-JAN-2006, i
DT 24-JAN-2006, e
DT 07-MAR-2006, e
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24-JAN-2006,
07-MAR-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AY750065; AAX51996.1; -; Genomic DNA.
GO; GO:0005739; C:mitochondrion; IEA.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone
NON TER
341
SEQUENCE 341 AA; 39646 MW; 5D1F0BAE2786B4A:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Phylogenetic analysis of the Drosophila robusta and melanica groups based on mitochondrial and nuclear DNA sequences."; Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthrop
Neoptera; Endopterygota; Di
Ephydroidea; Drosophilidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
Wang B.-C., Park J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang Y.-P.;
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Pred. No. 3
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Pred. No. 3.2e+02;
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entry version 3.

integrated into UniProtKB/TrEMBL

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RESULT 48
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groups based on mitochondrial and nuclear DNA sequences.";
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Phylogenetic analysis of the Drosophila robusta and melanica species groups based on mitochondrial and nuclear DNA sequences."; Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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24-JAN-2006, sequence version 1.
07-MAR-2006, entry version 3.
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SEQUENCE
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Ephydroidea; Drosophilidae;
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NADH dehydrogenase subunit 2 (Fragment)
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QZTNT9;
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                                                                                                                                                                                                                                              EMBL; AY750062; AAX51993.1; -; Genomic_DNA. GO; GO:0005739; C:mitochondrion; IEA.
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Distributed
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Mitochondrion; NAD; Oxidoreductase; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE. Wang B.-C., Park J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion
                                                                                                                                                                            Mitochondrion; NAD;
NON_TER 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang Y.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=65966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner membrane; multi-pass membrane protein (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY750064; AAX51995.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y.-P.
Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WMLSAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WMLSAMS 191
                                                                                                                                           341
341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 AA;
                                                                                                                                                                                                                                                                                                                        by the UniProt Consortium, see http://www.uniprot.org/terms
under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Park J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                341
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                                                                                                                                               39512 MW;
                                                                                                                                                                                                             Oxidoreductase;
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                                    84.2%;
85.7%;
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ae; Drosophila.
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Pred. No. 3.2e+02;
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                                                                                                                                               65E3CB198E6B59C4 CRC64;
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       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gao J.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gao J.-J.,
                                                                                                                                                                                                          Ubiquinone
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                                    3.2e+02;
                                                                     DB 2;
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RESULT 50
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ID Q2TNU1_9DIPT
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Q2TNU0_9D1
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Best Local S
Matches 6
"Phylogenetic analysis of the Drosophila robusta and melanica groups based on mitochondrial and nuclear DNA sequences."; Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol-
-!- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner multi-pass membrane protein (By similarity).
                                                                                                                                                                                                                                  24-JAN-2006, integrated into UniProtKB/T 24-JAN-2006, sequence version 1. 07-MAR-2006, entry version 3. NADH dehydrogenase subunit 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005739; C:mitochondrion; IEA. —
Mitochondrion; NAD; Oxidoreductase; Ubiquinone
NON_TER 341 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 groups based on mitochondrial and nuclear DNA sequences.";
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner me
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NADH dehydrogenase subunit 2 (Fragment)
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07-MAR-2006, entry version 3.
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                                                                                                    NUCLEOTIDE SEQUENCE. Wang B.-C., Park J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
Wang B.-C., Park J.,
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NCBI_TaxID=311474;
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                                                                                      Wang B.-C.,
Zhang Y.-P.;
                                                                                                                                                           Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                     Drosophila tsigana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang Y.-P.; "Phylogenetic analysis of the Drosophila robusta and melanica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                        Mitochondrion.
                                                                                                                                          NCBI_TaxID=65966;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multi-pass membrane protein (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                      J.,
                                                                                                                                                                                                                                                                                                                                                                                   191
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85.7%;
                                                                                                      Watabe H.-A.,
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                      Gao J.-J.,
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                                                                                                                                                                             Muscomorpha;
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                   membrane;
                                                                                                      H.-W.,
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Post-processing: Minimum Match
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1. /RMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*

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3. /RMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*

4. /RMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*

5. /RMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

6. /RMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*

7. /RMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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Match
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Patent No. 6309877

GENERAL INFORMATION:

APPLICANT: Chau, Raymond M. W.

TITLE OF INVENTION: Isolation and Use of Mot
FILE REFERENCE: 12592-2

CURRENT APPLICATION NUMBER: US/08/928,862

CURRENT FILING DATE: 1997-09-12

NUMBER OF SEQ ID NOS: 5

SOPTWARE: PatentIN Ver. 2.0

SEQ ID NO 4

LENGTH: 33

TYPE: PRT

ORGANISM: Homo sapiens

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 Sequence 4, Application US/09592018 Patent No. 6759389 GENERAL INFORMATION:
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Pred. No.
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CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US 09/633,447
PRIOR TILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 08/9928862
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 08/751225
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: US 60/026792
PRIOR APPLICATION NUMBER: US 60/026792
PRIOR APPLICATION NUMBER: US 60/026792
PRIOR FILING DATE: 1996-09-27
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CURRENT APPLICATION NUMBER: US/09/592,018
CURRENT FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 08/9928862
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 08/751225
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: US 60/026792
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Matches
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
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APPLICANT: Chau, Raymond M.W.

TITLE OF INVENTION: Solation and Use of Motoneurontropic Factors
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                                                                                              Patent No. 6433142
GENERAL INFORMATION:
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Patent No. 6841531
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NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
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TYPE: PRT
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INVENTION:
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                                  Gesner, Thomas G. Clark, Stephen C. Turner, Katherine
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Megakaryocyte Stimulating Factors
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GENERAL INFORMATION:
APPLICANT: Turn
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APPLICATION NUMBER: US 07/546,117
FILING DATE: 29-UN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617)876-11
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 18-JAN-19
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LENGTH: 46 amino acids
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/3:
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATA:
PRIOR APPLICATION DATA:
US 07/546,114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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CITY: Cambridge
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                                                                                                                  NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM
                                                                                                                                                    TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                  1 WMLSAFS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMINO ACID

OGY: linear
                                               STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                WMLSPFS
                  COUNTRY: U.S.A. ZIP: 02140
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                                                                                                 ADDRESSEE: Genetics Institute,
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87 CambridgePark Drive
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                                                                                                                                                                                                                    Turner, Katherine Clark, Stephen C.
                                                                                                                                                                     Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.8%;
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Pred. No. 15;
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RESULT 6
US-07-757-022B-72
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              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DECENT: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION DATA:
PATENT APPLICATION DATA:
PATENT APPLICATION DATA:
PATENT APPLICATION DATA:
PATENT APPLICATION NUMBER: US/07/643,502
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Sequence 72, App---
No. 643314/
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                STREET: 87 Cambridge
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                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
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LENGTH: 46 amino acids
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FILING DATE: 16-Apr-2002
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WMLSPFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                               Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                  87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gesner, Thomas G. Clark, Stephen C.
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Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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US-10-124-557-72
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INFORMATION FOR SEQ ID NO: 72
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 72, App.:.
No. 7030223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 7030223
GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
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NAME: CSerr, Luann
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FILING DATE: 29-JUN-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                         ZIP: 02140
COMPUTER READABLE FORM:
                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                     CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 WMLSPFS 117
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                                                              APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 87 Cambi
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                NAME: Cserr,
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                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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(617) 876-10: 72:
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08-AUG-1989
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 5190
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-124-557-72
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                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATE: 18-CAN-1991
PRIOR APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-CAN-1991
PRIOR APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
PRIOR APPLICATION NUMBER: US 07/390,901
FILING DATE: 108-AUG-1989
                                  INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 72:
                                                                                                                                      NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
TOPOLOGY: 1i
                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 86.8%;
Local Similarity 85.7%;
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 WMLSPFS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WMLSAFS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gesner, Thomas G.
Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                       (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                        GI 5190
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Query Match
Best Local Similarity
Thes 6; Conserve
                                                  Query Match
Best Local Similarity
Frieds 6; Conserve
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US-10-124-557-64
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                                                                                                                                      ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-124-557-64
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                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
TELEPHONE: (617)876-1170
TELEPAY: (617)876-5851
INFORMATION FOR SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-JUN-1990

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pateentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Turner, Katherine
Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 WMLSPFS 145
139 WMLSPFS 145
                                 1 WMLSAFS 7
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                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                        NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 87 CambridgePark Drive CITY: Cambridge
                                                                                                                                                                                                                               LENGTH: 372 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genetics Institute,
                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hewick, Rodney M. Gesner, Thomas G.
                                                                                    86.8%;
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                                                                   Score 33; DB 3;
Pred. No. 1.2e+02;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 2;
Pred. No. 1.2e+02;
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                                                                                                                                                           64:
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                                                                                                     Length 372;
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RESULT 11
US-10-124-557-68
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                                                                                                                                                            Sequence 68, Application US/10124557
Patent No. 7030223
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6433142
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
INCOLOR APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 87 Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                               189 WMLSPFS 195
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics Institute, Inc.
                            Jacobs,
Hewick,
                                                                                                Turner, Katheri
Clark, Stephen
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85.7%;
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Rodney M. Thomas G.
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                                                                                                                                       Katherine
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Pred. No. 1.4e+02;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Query Match
Best Local Similarity
Watches 6; Conserva
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-10-124-557-68
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                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-07-757-022B-66
                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                               Sequence 66, Application US/07757022B
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                  APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CBEAT, LUADIN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                       STREET: 87 Cambı
CITY: Cambridge
                                                                              COUNTRY:
                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 WMLSPFS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 WMLSAFS 7
                                                                  02140
                                                                                                                                                                                                                                                                                                                                               6433142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                Massachusetts
7: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 422 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617)876-1170
                                                                                                                                      87 CambridgePark Drive
                                                                                                                                                                                                                                                              Turner, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                               Genetics Institute,
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Pred. No. 1.4e+02;
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OPERATING SYSTEM:

SYSTEM: PC-DOS/MS-DOS PatentIn Release #1.0,

Version #1.25

US/07/757,022B

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Best Local Similarity
Watches 6; Conserve
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US-10-124-557-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 66, Application US/10124557 Patent No. 7030223 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 423 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 29-DEC-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 29-JUN-1
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: CSETT, LUANN
NAME: CSETT, LUANN
REGISTRATION NUMBER: 31,822
REGISTRATION NUMBER: GI 5190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1:
CLASSIFICATION:
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                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Turner, Katherine Clark, Stephen C.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                             STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                            ZIP: 02140
                                                                                                                                                                                                                                                                CITY: Cambridge
                                                                                                                                                                                                                                                                               STREET: 87 CambridgePark Drive
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                                                                                                                                                                                                                                                                                                                                                                                                        Jacobs, Kenneth
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85.7%;
                                                                                                                                                                                                                                                                                                   Genetics Institute, Inc.
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Pred. No. 1.4e+02;
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                                                                                                                          Version #1.25
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SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-124-557-66
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Best Local Similarity
Watches 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryoc
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION UMADR: US 07/643,502
FILING DATE: 18-JAN-1991
                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
                                                                                                FILING DATE: 29-DEC-1989
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FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
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REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Genetics Institute,
87 CambridgePark Drive
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                                          JMBER: US 07/390,901
08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Megakaryocyte Stimulating Factors
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Pred. No. 1.4e+02;
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REFERENCE/DOCKET NUMBER:

GI 5190

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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 54: US-10-124-557-54
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US-10-124-557-54
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Best Local Similarity
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                                                                                                                                    REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPAX: (617)976-5851
INFORMATION FOR SEQ ID NO: 54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Turner, Katherine Clark, Stephen C.
                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 WMLSPFS 236
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                                                                            TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Cambridge
STATE: Massachusetts
                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                              NAME: Cserr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 87 CambridgePark Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
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                                                                                               ; MOLECULE TYPE: protein US-07-757-022B-44
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US-07-757-022B-44
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                              Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
                                                                                                                                                                                               TELEFAX: (617)876-585
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT AFFILCATION NUMBER: US/07/751, VALUE APPLICATION NUMBER: US/07/751, VALUE FILING DATE: 19910910
CLASSIFICATION: 530
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 07/643,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1270 amino acids
                                                                                                                                                                                                                                       NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Cambridge STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                             ENGTH:
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6; Conserv
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   1 WMLSAFS
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                                                                                                                                              AMINO ACID
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87 CambridgePark Drive
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Clark, Stephen C.
Turner, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hewick,
                                                                                                                                                                                                                (617)876-5851
                                   Conservative
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                                                                                                                                 linear
                                                                                                                                                                                                                               (617)876-1170
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                                                86.8%;
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85.7%;
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Pred. No.
                                                Score 33; DB 2;
Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                               5190
                                   Mismatches
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1.5e+02;
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                                                               Length 1270;
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1037 WMLSPFS 1043

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RESULT 18
US-07-757-022B-42
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                                                                                                                          Sequence 42, Application US/07757022B Patent No. 6433142 GENERAL INFORMATION:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 44:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-JUN-1990

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CBERT, LUBRIN REGISTRATION NUMBER: 31,822
REFERENCE/DOKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                            1037 WMLSPFS 1043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Turner, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       1 WMLSAFS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1270 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDRESSEE: Genetics Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/10124557
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ilarity 85.7%;
Conservative
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Gesner, Thomas G.
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Pred. No. 4.2e+02;
0; Mismatches 1
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US-10-124-557-42
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Best Local Similarity bo...
""" hes 6; Conservative
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Patent No. 7030223
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 07/545,...
FILING DATE: 29-UN-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/457,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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STREET: 87 Cambr
CITY: Cambridge
STATE: Massachus
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release ""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: AMINO ACID
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ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                TITLE OF INVENTION: Megakaryocyte Stimulating NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                   APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
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                                                                    CITY: Cambridge
STATE: Massachusetts
                                                         COUNTRY: U.S.A.
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87 CambridgePark Drive
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                                                                                                                                                                                                  Hewick, Rodney M. Gesner, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/07/757,022B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42:
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Pred. No. 4.4e+02
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-124-557-42
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAL PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-0AN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,512
FILING DATE: 18-0AN-1991
PRIOR APPLICATION NUMBER: US 07/546,114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 142, Application US/07757022B Patent No. 6433142 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 86.8%;
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M.
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 CITY:
                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1078 WMLSPFS 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                   Massachusetts: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143
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Pred. No. 4.4e+02;
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Query Match
Best Local Similarity
Marches 6; Conserva
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-757-022B-142
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US-10-124-557-142
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APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:

NAME: CBert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPAX: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 142:
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LENGTH: 1313 amino aci
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 29-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                            FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                          CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, '
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1080 WMLSPFS 1086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Megakaryocyte Stimulating Factors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WMLSAFS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts COUNTRY: U.S.A.
REFERENCE/DOCKET NUMBER: GI 5190 COMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Cambridge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genetics Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/10124557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUN-1990
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Pred. No. 4.4e+02;
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                                                                                                                                                                                                                                                                                                                                                         Version
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(617)876-1170

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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 142: US-10-124-557-142
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US-07-757-022B-50
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                                                                                                                                                                                           FILING DATE: 19910910

FILING DATE: 19910910

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
PRIOR APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAMB: CSett, LUAIN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
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INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 amino acids
                                                                                                                                                TELEFAX: (617)876-5851 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1314 amino aci
TYPE: AMINO ACID
TYPE: AMINO ACID
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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Local Similarity 85.7%;
les 6; Conservarium
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Massachusetts
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87 CambridgePark Drive
                                                                                      314 amino acids
                              linear
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Pred. No. 4.4e+02;
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Best Local Similarity
Matches 6; Conserv:
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US-10-124-557-50
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GENERAL INFORMATION:
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Sequence 50, Appri
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Best Local Similarity
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                                                                                                                                                                                                                                                                             TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/124,557
PILING DATE: 16-Apr-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
PILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
PILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
PILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
PILING DATE: 08-AUG-1989
APPLICATION NUMBER: US 07/390,901
PILING DATE: 08-AUG-1989
APPLICATION NUMBER: US 07/390,901
PILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Turner, Katherine
Clark, Stephen C.
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 1081 WMLSPFS 1087
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                                     1 WMLSAFS 7
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STATE: Massachusetts
                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                           LENGTH: 1314 amino acids
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                                                                        Conservative
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                                                                                        86.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rodney M.
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Pred. No. 4.4e+02;
                                                                        Score 33; DB 3;
Pred. No. 4.4e+02;
0; Mismatches 1
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                                                                                                                                                                     50:
                                                                                                            Length 1314;
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                                                                          Gaps
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RESULT 25
US-07-757-022B-60
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                                                                                                                             Sequence 60, Application US/07757022B Patent No. 6433142 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 46, Ap
Patent No. 6433
                                                                                                                                                                                                                                                                                                                                                        Query Match 86.8%;
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
PRIOR APPLICATION NUMBER: US 07/390,901
PRIOR APPLICATION NUMBER: US 07/390,901
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M. TITLE OF INVENTION: Megakaryoc NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617)876-585: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1320 amino aci
TYPE: AMINO ACID
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NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 8/ Cambridge
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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STATE: Massachusetts
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                                                                                                                                                                                                                                                                           1087 WMLSPFS 1093
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    Megakaryocyte Stimulating Factors
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Pred. No. 4.4e+02;
0; Mismatches 1;
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; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-757-022B-60
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US-10-164-595-58
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                                                                             ; ORGANISM: Homo sapiens
US-10-164-595-58
                                                                                                                                                                                                                                                                                             Sequence 58, Application US/10164595 Patent No. 6657054 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                SEQ ID NO 58
LENGTH: 1320
   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                   FILE REFERENCE: 1U 103 R1
CURRENT APPLICATION NUMBER: US/10/164,595
CURRENT FILING DATE: 2002-06-10
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                           APPLICANT: OriGene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 amino aci
                                                                                                                   TYPE: PRT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 29-DEC-:
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PRIOR APPLICATION UDATA:
APPLICATION UMBER: US 07/643,502
FILING DATE: 18-JAN-1991
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APPLICATION NUMBER: US 07/546,114
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STATE: Massachusetts
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87 CambridgePark Drive
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     Conservative
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                    86.8%;
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     Score 33; DB Pred. No. 4.4e 0; Mismatches

 Mismatches

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Pred. No. 4.4e+02;
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 Db ...
4.4e+02;
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                                         Length 1320;
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         Indels
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     Gaps
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RESULT 27
US-10-124-557-46
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                                                  RESULT 28
US-10-124-557-60
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Sequence 60, Application US/10124557 Patent No. 7030223 GENERAL INFORMATION:
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Patent No. 7030223
GENERAL INFORMATION:
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                   Query Match 86.8%;
Best Local Similarity 85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617)876-58: INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
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Clark, Stephen
                                                                                                                              1087 WMLSPFS 1093
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                             1 WMLSAFS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WMLSAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1320 amino acids
                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EE: Genetics Institute,
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                           (617)876-5851
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                                                                                                                                                                                                                     Score 33; DB 3;
Pred. No. 4.4e+02;
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RESULT 29
US-07-757-022B-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                    GENERAL INFORMATION:
APPLICANT: Geener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 1330 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 6; Conserv
                STREET: 87 CambridgePark Drive CITY: Cambridge
                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                       1087 WMLSPFS 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein SEQ ID NO: 60:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                      1 WMLSAFS 7
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NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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Massachusetts
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                                                        Genetics Institute, Inc
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Clark, Stephen C
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Hewick, Rodney M.
Gesner, Thomas G.
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85.7%;
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Pred. No. 4.4e+02;
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COUNTRY: U.S.A.

02140

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RESULT 30
US-10-124-557-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity 85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)876-5851 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390
APPLICATION NUMBER: US 07/390
PILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1354 amino acids
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APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
PRIOR TENER OF US 07/457,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07/757,022E
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1. CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palan-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                      ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: PBatentin Release #1.0, Version

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Turner, Katherine
Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1121 WMLSPFS 1127
                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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GY: linear
                                                                                                                                                                          STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                     STREET: 87 CambridgePark Drive CITY: Cambridge
APPLICATION NUMBER: US/10/124,557
                                                                                                                                                                                                                                                               ADDRESSEE: Genetics Institute, Inc
                                                                                                                                                                                                                                                                                                                                                Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 07/390,901
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Pred. No. 4.5e+02;
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Query Match
Best Local Similarity
"""hes 6; Conserve
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US-07-757-022B-40
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               SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-CAM-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNU-1990
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNU-1990
PRIOR APPLICATION NUMBER: US 07/457,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gesner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OCCUMANTS. Patents Paleon #100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
APPLICATION NUMBER: US 0 FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 87 Cambı
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1354 amino acids
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REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 16-Apr-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/546,114 FILING DATE: 29-JUN-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Massachusetts
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85.7%;
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Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1354;
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RESULT 32
US-10-124-557-40
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Patent No. 7030223
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 40:
              INFORMATION FOR SEQ ID NO: 40: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS LENGTH: 1361 amino ac
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ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-JUN-1990

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

APPLICATION NUMBER: US 07/390,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1128 WMLSPFS 1134
                                                                     NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Turner, Katherine
Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 WMLSAFS 7
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                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                           TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/10124557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.8%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics Institute, Inc.
amino acids
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Pred. No. 4.5e+02;
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US-07-757-022B-52
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                                                                               US-07-757-022B-52
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Patent No. 6433142
                                                                                                                             TELEPHONE: (617)876-1170
TELEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1363 amino acids
TYPE: AMINO ACID
TOPOCO: 11802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/643,502
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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Best Local :
                                      Query Match
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                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                               TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 29-JUN-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 86.8%;
Local Similarity 85.7%;
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Cambridge
STATE: Massachusetts
Local Similarity 85.
                                                                                                                                                                                                                                                                                    NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1128 WMLSPFS 1134
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                                                                                               protein
  86.8%; Score 33; DB
85.7%; Pred. No. 4.50
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 07/546,114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                  4.5e+02;
                                        DB 2;
                                    Length 1363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
    Indels
    0;
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    0;
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WMLSAFS

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RESULT 35
US-07-757-022B-2
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US-10-124-557-52
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                                                                                                                                                                                                                                                                                                                      US-10-124-557-52
Sequence 2, Application US/07757022B
Patent No. 6433142
GEMERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 52, Applicati Patent No. 7030223 GENERAL INFORMATION:
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02140

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYBE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/124,557

FILING DATE: 16-Apr-2002

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            Local Similarity 85.7%; hes 6; Conservation
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                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                           1130 WMLSPFS 1136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                  1 WMLSAFS 7
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STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1363 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/10124557
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Hewick, Rodney M.
Gesner, Thomas G.
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                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                           Score 33; DB 3;
Pred. No. 4.5e+02;
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Query Match
Best Local Similarity
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US-07-757-022B-62
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                                                                                                                                                                                                                   Sequence 62, Application US/07757022B Patent No. 6433142
                                                                                                                          GENERAL INFORMATION:
APPLICANT: Geener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 2:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1404 amino aci
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 1
FILING DATE: 18-JAN-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                        TITLE OF INVENTION:
NUMBER OF SEQUENCES:
STREET: b, STREET: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/457,196 FILING DATE: 29-DEC-1989
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)GY: linear
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                                 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1404 amino acids
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Katherine
Rodney M.
                                                                                          Megakaryocyte Stimulating Factors: 143
                                                                                                                                                                                                                                                                                                                                                                                                                        86.8%;
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Pred. No. 4.7e+02;
0; Mismatches 1
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COMPUTER READABLE FORM:

MEDIUM TYPE: ZIP: 02140

Floppy disk

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

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                                                                                                                                     ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-164-595-78
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US-10-164-595-78
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APPLICANT: OriGene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REFERENCE: 1U 103 R1
CURRENT APPLICATION NUMBER: US/10/164,595
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                 Sequence 78, Application US/10164595
Patent No. 6657054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
                                                                   Matches
                                                                                       Best
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 62:
                                                                                                                                                                                        LENGTH: 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
APPLICATION NUMBER: US 07/390,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19910910
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                    Local Similarity
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1171 WMLSPFS 1177
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AMINO ACID
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                                                                   Conservative
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85.7%;
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                                                                 Score 33; DB 2; Le
Pred. No. 4.7e+02;
0; Mismatches 1;
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                                                                                                    Length 1404;
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Sequence 1, Application US/09298970A
Patent NO. 6743774
GENERAL INFORMATION:
APPLICANT: Jay, Gregory D.
TITLE OF INVENTION: TRIBONECTINS
FILE REFERENCE: 21486-026
CURRENT APPLICATION NUMBER: US/09/298,970A
CURRENT FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FAStSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1404
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US-09-298-970A-1
                                                                                                                                                                                 ; Sequence 1, Application US/09556246 ; Patent No. 7001881
                                                                                                                                                                                                                        US-09-556-246-1
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                                                                                                      GENERAL INFORMATION:
APPLICANT: Gregory D. Jay
TITLE OF INVENTION: tribonectins
FILE REFERENCE: 21486-026cip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.,
Yorches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Jay, Gregory D.
APPLICANT: INVENTION: Tribonectin Polypeptides and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09897188 Patent No. 6960562
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/897,188
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: 09/298,970
PRIOR FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: 09/556,246
DRIOR STILL CATTON NUMBER: 09/556,246
FILE REFERENCE: 21486-026cip
CURRENT APPLICATION NUMBER: US/09/556,246
CURRENT FILING DATE: 2000-04-24
PRIOR APPLICATION NUMBER: USSN 09/298/970
PRIOR FILING DATE: 199-04-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-04-24
NUMBER OF SEQ ID NOS: 34
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ORGANISM: Homo sapiens
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85.7%;
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Pred. No. 4.7e+02;
0; Mismatches 1
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Pred. No.
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US-10-124-557-2
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Best Local Similarity 85.7%;
Matches 6; Conservative
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LENGTH: 1'
                                      Matches
                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1171 WMLSPFS 1177
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COMPUTER READABLE FORM:
                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: (
                                                                                                                                                                                                                                                                               NAME: Ceerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Turner, Katherine
                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WMLSAFS 7
                                      9
   WMLSAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Cambridge
                                                                                                                                                                                             LENGTH: 1404 amino acids
                                                                                                                                                                                                                                                TELEFAX: (617)876-5851
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
                                                                                                                                                                                                                                                                    (617)876-1170
                                                     86.8%;
85.7%;
                                                                                                                           SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 3;
Pred. No. 4.7e+02;
0; Mismatches 1
                                    0;
                                  Score 33; DB 3;
Pred. No. 4.7e+02;
0; Mismatches 1
                                                                                                                           NO:
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                                                                                                                                                                                                                                                                                                     5190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1404;
                                    1; Indels
                                                                   Length 1404;
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                                    Gaps
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TOPOLOGY: linear;

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-10-124-557-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 42
US-10-124-557-62
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                                                                                                 RESULT 43
US-09-949-016-10827
                                                                                                                                                                                    밁
Sequence 10827, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 62, Applicati
Patent No. 7030223
GENERAL INFORMATION:
APPLICANT: Turn
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-JUN-1990

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1171 WMLSPFS 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
                                                                                                                                                                                1171 WMLSPFS 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                         1 WMLSAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,822 REFERENCE/DOCKET NUMBER: GI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Cserr,
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                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jacobs, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Turner,
                                                                                                                                                                                                                                                                                 86.8%;
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Pred. No. 4.
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4.7e+02;
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US-09-107-532A-4889
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US-09-949-016-10827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4889, Application US/09107532A

Patent No. 6583275

Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version SEQ ID NO 10827
LENGTH: 1411
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
                                                                                                                          INFORMATION FOR SEQ ID NO: 4889:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: J14 /2 , 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
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les 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1178 WMLSPFS 1184
                                     MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Waltham
                                                                                                                                                                                                                     TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                     ORGANISM: Enterococcus
                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                      TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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85.7%;
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Pred. No. 4.7e+02;
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US-09-252-991A-22359
                                           CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR TLING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/118,206,
                                                                                                                                                                                                                                                                                                                                                                          US-09-712-363-283
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-252-991A-22359
                                                                                                                                                                                                                                                                                                                   Sequence 283, Application US/09712363 Patent No. 6892139 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
SEQ ID NO 22359
LENGTH: 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22359, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERADEFITTICS
                                                                                                                                                                                                        APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
FILE REFERENCE: 07419-032001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
                                   PRIOR FILING DATE: 1999-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: UNSURE LOCATION: (182)
OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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LOCATION: (B) LOCATION 1...103
SEQUENCE DESCRIPTION: SEQ ID NO: 4889:
APPLICATION NUMBER: 60/126,593 FILING DATE: 1999-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 WMLSAIS 240
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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BY
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                                                                                                                                                                                                                                   COMPARATIVE ANALYSIS
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Sequence 99, Application US/09586106D

Patent No. 6720479

GENERAL INFORMATION:

APPLICANT: Wright, David A.

APPLICANT: Voytas, Daniel F.

TITLE OF INVENTION: PLANT RETROCLEMENTS AND METHODS RELATED THERETO

FILE REFERENCE: P-1065A

CURRENT APPLICATION NUMBER: US/09/586,106D

CURRENT FILING DATE: 2003-02-07

PRIOR APPLICATION NUMBER: 60/087,125

PRIOR APPLICATION NUMBER: 09/322,478

PRIOR FILING DATE: 1998-05-29

PRIOR FILING DATE: 1999-05-28

RUMBER OF SEQ ID NOS: 190
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US-09-489-039A-7403
j Sequence 7403, Application US/09489039A
j Patent No. 6610836
j GENERAL INFORMATION:
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US-09-586-106D-99
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; TYPE: PRT
; ORGANIZM: Klebsiella pneumoniae
US-09-489-039A-7403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7403
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Matches
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SOFTWARE: PRETSEQ for Windows Version 4.0
SEQ ID NO 283
LENGTH: 280
TYPE: PRT
                               SEQ ID NO 99
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/165,124 PRIOR FILING DATE: 1999-11-12
                                                        SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 229
TYPE: PRT
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Local Similarity 85.7%;
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APPLICATION NUMBER: 60/
FILING DATE: 1999-05-14
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Pred. No. 1.4e+02;
2; Mismatches (
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Pred. No. 2.2e+02;
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US-09-107-532A-3700
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Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 190
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 99
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APPLICANT: Voytas, Daniel F.
APPLICANT: Voytas, Daniel F.
INTER OF INVENTION: PLANT RETROELEMENTS AND METHODS RELATED THERETO
FILE REFERENCE: P-1065A
CURRENT APPLICATION NUMBER: US/10/799,870
CURRENT FILING DATE: 2004-03-12
PRIOR APPLICATION NUMBER: US/09/586,106
PRIOR FILING DATE: 2003-02-07
PRIOR FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: 60/087,125
PRIOR PRIOR DATE: 1998-05-29
PRIOR PILING DATE: 1998-05-29
PRIOR FILING DATE: 1998-05-28
PRIOR FILING DATE: 1999-05-28
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TYPE: PRT
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
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les 5; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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1; Mismatches

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Pred. No. 1.8e+02;
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1.8e+02;
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APPLICATION NUMBER: 60/051571

ATTONNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
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Result
No.
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Maximum
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Maximum
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Perfect score:
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Query
Match
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1. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US110B_PUBCOMB.pep:*

6. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
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of the total score distribution
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78-10-941-343-6

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78-10-858-545-4

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78-10-858-144-4

78-10-541-343-1

78-10-97-143-16893

78-10-124-557-18

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S-10-124-557-72

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S-10-124-557-64

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US-10-541-343-3
; Sequence 3, Application US/10541343
; Publication No. US20060052299A1
; GENERAL INFORMATION:
APPLICANT: Chau, Raymond Ming Wah
APPLICANT: Ko, Pui-Yuk Dorochy
TITLE OF INVENTION: MNTF Peptides and Compositi
FILE REFERENCE: 2001-103US
; CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US/10/541,343
; CURRENT FILING DATE: 2005-07-05
PRIOR RPLICATION NUMBER: PCT/US2004/001468
PRIOR APPLICATION NUMBER: 60/441,722
PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.3
; LEUGTH: 7
; TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-10-541-343-3
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                                                Query Match
Best Local
Matches
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                                                Similarity 7; Conserv
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                                              100.0%; ilarity 100.0%; Conservative 0;
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US-10-325-175-307311
US-10-335-977-9307
US-09-864-761-45039
US-10-325-115-266020
US-10-425-115-266021
US-10-425-115-266021
US-10-425-115-266021
US-10-424-599-218746
US-10-125-115-28417
US-09-833-245-1395
US-10-125-479-24
US-10-98-33-245-1395
US-10-1264-096-1396
US-11-264-096-1396
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US-10-424-599-23057
US-10-424-599-230586
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US-11-425-115-3318
US-10-425-115-394547
US-10-425-115-39456
US-10-425-115-39456
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Pred. No.
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                                                 Mismatches
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3077, Ap
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US-10-541-343-6

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RESULT 4
US-10-858-545-4
; Sequence 4, Application US/10858545
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; OTHER INFORMATION: Synthetic peptide
US-10-541-343-6
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US-09-989-481-4
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                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
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LENGTH: 13
TYPE: PRT
ORGANISM: Artificial
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Publication No. US20060052299A1
GENERAL INFORMATION:
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Best Local
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PRIOR APPLICATION NUMBER: PCT/US2004/001468
PRIOR FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: 60/441,722
PRIOR FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 7
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APPLICANT: Ko, Pui-Yuk Dorothy
TITLE OF INVENTION: MNTF Peptides and Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 08/9928862
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 08/751225
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: US 60/026792
PRIOR FILING DATE: 1996-09-27
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CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US 09/633,447
PRIOR FILING DATE: 2000-08-07
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CURRENT APPLICATION NUMBER: US/10/541,343
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TITLE OF INVENTION: Isolation and Use of Motoneurontropic Factors
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100.0%; Pred. No. 6.8;
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RESULT 6 US-10-858-543-4

Sequence 4, Application US/10858543 Publication No. US20040266691A1 GENERAL INFORMATION:

Raymond M.W.

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                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 33
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APPLICANT: Chau, Raymond M.W.
TITLE OF INVENTION: Isolation and Use of Motoneurontropic Factors
FILE REFERENCE: 12592-3
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/858,286
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US/09/592,018
PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 08/9928862
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 08/751225
PRIOR APPLICATION NUMBER: US 08/751225
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PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 08/9928862
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PRIOR APPLICATION NUMBER: US 60/026792
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PRIOR APPLICATION NUMBER: US 08/751225
PRIOR FILING DATE: 1996-11-15
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CURRENT FILING DATE: 2004-06-01
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TITLE OF INVENTION: Isolation and Use of Motoneurontropic Factors
FILE REFERENCE: 12592-3
                                                                                                                                                                                                                                                           PRIOR FILING DATE:
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NUMBER OF SEQ ID NOS: 5
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TYPE: PRT
ORGANISM: Homo Sapiens
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WMLSAFS 18
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Pred. No.
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US-10-858-543-4
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CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US/09/592,018
PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 08/9928862
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 08/751225
PRIOR APPLICATION NUMBER: US 08/751225
PRIOR FILING DATE: 1996-11-15
PRIOR PILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: US 60/026792
PRIOR APPLICATION NUMBER: US 60/026792
PRIOR FILING DATE: 1996-09-27
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PRIOR FILING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 08/9928862
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: US 08/751225
PRIOR APPLICATION NUMBER: US 60/026792
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Best Local S
Matches 7
                                                                               Sequence 1, Application US/10541343
Publication No. US20060052299A1
GENERAL INFORMATION:
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LENGTH: 3
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SEQ ID NO 4
LENCTH: 33
TYPE: PRT
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Publication No. US20060025565A1
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APPLICANT: Chau, Raymond Ming Wah
APPLICANT: Ko, Pui-Ywir Dorothy
TITLE OF INVENTION: MYTH Dorothy
FILE REFERENCE: 2001-103US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
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TITLE OF INVENTION: Isolation and Use of Motoneurontropic Factors
FILE REFERENCE: 12592-3
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CURRENT FILING DATE: 2004-06-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 38; DB 5; Local Similarity 100.0%; Pred. No. 6.8; hes 7; Conservative 0. Minner.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
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                                                                                                                                                                                                                                                                                         1 WMLSAFS 7
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                                                                                                                                                                   US-11-097-143-16893
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR APPLICATION NUMBER: 60/175,693
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                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16893, Application US/11097143
Publication No. US200502085881
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 38; Best Local Similarity 100.0%; Pred. No. Matches 7; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.3 SEQ ID NO 1
                                                                               Matches
                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
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PRIOR FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US2004/001468 PRIOR FILING DATE: 2004-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/541,343
CURRENT FILING DATE: 2005-07-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                       ORGANISM: DROSOPHILA
                                                                                                                                                                                                                               LENGTH: 1760
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966
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WMVSAFS
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                                                                               Conservative
972
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                                                                                                 Score 35; DB 6;
Pred. No. 8.4e+02;
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                                                                                                                       Length 1760;
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RESULT 10 US-10-424-599-187845

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US-10-124-557-18
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US-10-424-599-187845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5323)B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 187845
LENGTH: 103
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Publication No. US20020137894A1
GENERAL INFORMATION:
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Best Local (
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                  APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
APPLICATION UNMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Turner, Katherine
Clark, Stephen C.
REFERENCE/DOCKET NUMBER: GI 5190 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genetics Institute, Inc
STREET: 87 CambridgePark Drive
                                           REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
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Hewick, Rodney M.
Gesner, Thomas G.
                                                                    Cserr,
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85.7%;
                                                                    Luann
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, MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: US-11-169-232-18
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                   INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino aci
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nes 6; Conserv
                                                                                                                                    TELEPAX: (617)876-5851
                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/11/169,232
FILING DATE: 28-Jun-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Turner, Katherine
Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Megakaryocyte Stimulating Factors
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                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: linear
                                                                                                                                                                                                    NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/457,196 FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 28-Jun-2005 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/11169232
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87 CambridgePark Drive
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Pred. No.
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RESULT 13
US-09-925-301-1452
; Sequence 1452, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
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US-10-124-557-72
; Sequence 72, Application US/10124557
; Publication No. US20020137894A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 61
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (6)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION UNMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Turner, Katherine
Clark, Stephen C.
                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 WMLSPFS 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ហ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WMLSAFS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                          CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WMLSPFS 11
                                                                                                                                                             ZIP: 02140
                                                                                                                                                                                                                                 STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                   ADDRESSEE: Genetics Institute, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                       Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 3;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                         Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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TOPOLOGY: linear

MOLECULE TYPE: Protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-124-557-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
%%**hes 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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US-11-169-232-72
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Publication No. US20060025570A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Unn-2005
CLASSIFICATION: <und>CUnknown>PRIOR APPLICATION NUMBER: US/10/124,557APPLICATION NUMBER: US/10/124,557FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US/07/643,502APPLICATION NUMBER: US/07/643,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Turner, Katherine
Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 WMLSPFS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WMLSAFS 7
                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 237 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Cserr, Luann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 4;
Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inc.
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Query Match
Best Local Similarity
~~~hes 6; Conserve
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  8
   US-10-124-557-64
   RESULT 16
   US-11-169-232-72
  Sequence 64, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
   TELEFAX: (617)876-58
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
                                    INFORMATION FOR SEQ ID NO: 64:
   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: PATENTIAL RELEASE #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/10/124,557

APPLICATION NUMBER: US/10/124,557
   APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
   TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 8
   TELEFAX: (617)876-5851
   FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
   Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
  APPLICANT: Turner, Katnerine Clark, Stephen C.
   ATTORNEY/AGENT INFORMATION:
                    SEQUENCE CHARACTERISTICS:
  CORRESPONDENCE ADDRESS:
  111 WMLSPFS 117
   1 WMLSAFS 7
  APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
  STATE: Massachusetts
  TYPE: amino acid
  REGISTRATION NUMBER: 31,822
  COUNTRY: U.S.A.
   CITY: Cambridge
   STREET:
  NAME: Cserr,
   ADDRESSEE:
  LENGTH: 237 amino acids
   Conservative
   87 CambridgePark Drive
372 amino acids
   Genetics Institute,
  86.8%;
  Luann
   SEQ ID NO:
   0;
  Score 33; DB 6; Length 237; Pred. No. 3.3e+02;
   Mismatches
   Indels
   0;
  Gaps
   0
```

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TOPOLOGY: linear
;
MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-124-557-64
  В
  Ś
   US-11-169-232-64
   RESULT 17
   US-11-169-232-64
   Sequence 64, Application US/11169232 Publication No. US20060025570A1
  Matches
  Query Match
                                 Query Match
Matches
  INFORMATION FOR SEQ ID NO: 64:
  GENERAL INFORMATION:
Local Similarity nes 6; Conserv
  Local Similarity 85.
   APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
   APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
  REFERENCE/DOCKET NUMBER: GI 5190 TELECOMMUNICATION INFORMATION:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  SEQUENCE CHARACTERISTICS:
   CORRESPONDENCE ADDRESS:
   NUMBER OF SEQUENCES:
   TITLE OF INVENTION: Megakaryocyte Stimulating Factors
  139 WMLSPFS 145
  1 WMLSAFS 7
   APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
   NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
  STATE: Massachusetts COUNTRY: U.S.A.
  TYPE: amino acid
  LENGTH: 372 amino acids
   APPLICATION NUMBER: US 07/457,196 FILING DATE: 29-DEC-1989
  CITY: Cambridge
   STREET: 87 CambridgePark Drive
  TELEPHONE: (617)876-5851
  ZIP: 02140
   ADDRESSEE:
 Conservative
  Turner, Katherine Clark, Stephen C.
  Jacobs, Kenneth
  Hewick, Rodney M.
Gesner, Thomas G.
                 86.8%;
  86.8%;
  (617)876-1170
   Genetics Institute,
  0; Mismatches
 0; Mismatches
  Score 33;
Pred. No.
                 Score 33; DB 6;
Pred. No. 5e+02;
  64:
   64:
  5e+02;
                                 DB 6;
   Inc.
   DB 4;
  Version #1.25
   Length 372;
                                 Length 372;
  Indels
   Indels
   o
;
   0,
  Gaps
 Gaps
 0
   0,
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-124-557-68
  RESULT 19
US-11-169-232-68
   뭐
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  밁
  δ
   RESULT 18
US-10-124-557-68
   Sequence 68, Application US/10124557 Publication No. US20020137894A1 GENERAL INFORMATION:
Sequence 68, Application US/11169232
Publication No. US20066025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
  Matches
  Query Match
  INFORMATION FOR SEQ ID NO: 68:
  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-JUN-1990

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

ATTORNEY/AGENT INFORMATION:
   Local Similarity
  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
   TELEFAX: (617)876-5851
  ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
   SEQUENCE CHARACTERISTICS:
  CORRESPONDENCE ADDRESS:
  TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
   APPLICANT: Turner, Katherine Clark, Stephen C.
  189
   139
  1 WMLSAFS 7
  6
  WMLSPFS 195
   WMLSPFS
   WMLSAFS
  STREET: 87 CambridgePark Drive CITY: Cambridge
   LENGTH: 422 amino acids
TYPE: amino acid
   NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
  STATE: Massachusetts
  COUNTRY: U.S.A.
  ADDRESSEE: Genetics Institute, Inc
  Conservative
   Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
   145
  86.8%;
  0
   Score 33; DB 4;
Pred. No. 5.6e+02;
  Mismatches
   GI 5190
  68:
  1; Indels
  Length 422;
  0;
  Gaps
  0
  밁
   S
   Best Loc
Matches
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RESULT 20
US-10-124-557-66
  US-11-169-232-68
  Sequence 66, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
  Query Match
   INFORMATION FOR SEQ ID NO: 68: SEQUENCE CHARACTERISTICS:
   APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/446,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
   Local Similarity hes 6; Conserv
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
  TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
  COMPUTER READABLE FORM:
  TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
  189 WMLSPFS 195
  1 WMLSAFS 7
  ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive CITY: Cambridge
   NABE: Cserr, Luann
REGISTRATION NUMBER: 31,822
   APPLICATION NUMBER: US/11/169,232 FILING DATE: 28-Jun-2005
  STATE: Massachusetts COUNTRY: U.S.A.
   TYPE: amino acid
  MEDIUM TYPE: Floppy disk
   LENGTH: 422 amino acids
  Conservative
  Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
  Clark, Stephen C.
  86.8%;
  0,
  Score 33; DB 6; 1
Pred. No. 5.6e+02;
0; Mismatches 1
   68
                        Inc.
  Inc.
  Length 422;
  Indels
  0
  Gaps
```

FILING DATE: 28-Jun-2005

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   RESULT 21
US-11-169-232-66
   US-10-124-557-66
  Sequence 66, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
   Matches
   Best Local Similarity
  Query Match
  INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
  Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
   REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 1EM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
   ATTORNEY/AGENT INFORMATION:
   PRIOR APPLICATION DATA:
  190 WMLSPFS 196
   1 WMLSAFS 7
  APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
   ٥,
   CITY: Cambridge
STATE: Massachusetts
  NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
   APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: «Unknown»
  CITY: Cambridge
STATE: Massachusetts
   COUNTRY: U.S.A. ZIP: 02140
  STREET: 87 CambridgePark Drive
  TYPE: amino acid
  COUNTRY: U.S.A.
APPLICATION NUMBER: US/11/169,232
  ADDRESSEE: Genetics Institute, Inc.
  LENGTH: 423 amino acids
   Conservative
  Turner, Katherine
Clark, Stephen C.
  86.8%;
   0; Mismatches
  Score 33; DB 4;
Pred. No. 5.6e+02;
   ۲,
  Length 423;
   <u>,</u>
   Gaps
   0
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  Ş
  RESULT 22
US-10-124-557-54
   US-11-169-232-66
  Query Match
Best Local Similarity 85...
"""hes 6; Conservative
   Sequence 54, Applicati
Publication No. US2002
GENERAL INFORMATION:
  TELEFAX: (617)876-58
INFORMATION FOR SEQ ID NO: 66:
  APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
   CCARSIFICATION: «Unknown»
  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
   TELEFAX: (617)876-5851
  PRIOR APPLICATION DATA:
  APPLICANT: Turner, Katherine
Clark, Stephen C.
  SEQUENCE CHARACTERISTICS:
  PRIOR APPLICATION DATA:
   CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES: 143
   TITLE OF INVENTION: Megakaryocyte Stimulating Factors
   190 WMLSPFS 196
  1 WMLSAFS 7
  NAME: Ceerr, Luann
NAME: Ceerr, Luann
REGISTRATION NUMBER: 31,822
   ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive CITY: Cambridge
  APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991 APPLICATION NUMBER: US 07/546,114
  LENGTH: 423 amino acids TYPE: amino acid
  APPLICATION NUMBER: US 07/546,114 PILING DATE: 29-JUN-1990
   APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002
   CLASSIFICATION: <Unknown>
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
   COUNTRY: U.S.A.
  STATE: Massachusetts
   FILING DATE: 18-JAN-1991
  APPLICATION NUMBER: US 07/643,502
  Application US/10124557
No. US20020137894A1
   Hewick, Rodney M. Gesner, Thomas G.
   Jacobs, Kenneth
  Genetics Institute, Inc.
   86.8%;
85.7%;
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   Score 33; DB 6;
Pred. No. 5.6e+02;
  Mismatches
   Length 423
  0
  Gaps
  0
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LENGTH: 463 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-10-124-557-54
  US-11-169-232-54
  RESULT 23
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  Sequence 54, Application US/11169232 Publication No. US20060025570A1 GENERAL INFORMATION:
   Matches
   Query Match 86.8%;
Best Local Similarity 85.7%;
   TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 54:
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Oun-2005
CLASSIFICATION NUMBER: US/11/169,232
FILING DATE: 28-Oun-2005
CLASSIFICATION OLORIA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US/07/643,502
FILING DATE: 18-OAN-1991
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-OAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/546,119
FILING DATE: 09-AUG-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989 ATTORNEY/AGENT INFORMATION:
  TELEPHONE: (617)876-1170
  CORRESPONDENCE ADDRESS:
   TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
   TELECOMMUNICATION INFORMATION:
  APPLICANT: Turner, Katherine
   230 WMLSPFS 236
   1 WMLSAFS 7
   6; Conservative
                                      NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
   STATE: Massachusetts COUNTRY: U.S.A.
   NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
   CITY: Cambridge
   ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
TELEPHONE:
   Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
  Clark, Stephen C.
   Score 33; DB 4;
Pred. No. 6e+02;
   Mismatches
   5190
  5190
  DB 4; Length 463
   1; Indels
   0,
   Gaps
   0
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밁
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   US-10-038-694-3
   US-11-169-232-54
  US-09-802-207-27
  US-10-038-694-3
  GENERAL INFORMATION:
APPLICANT: Dixon, Er
APPLICANT: Hutchins
APPLICANT: Kuettner
   NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
   Query Match
Best Local Similarity
Matches 6; Conserv
   Sequence 3, Application US/10038694 Publication No. US20030180948A1
  GENERAL INFORMATION:
  Sequence 27, Application US/09802207
Publication No. US20020086824A1
  Matches
  Query Match
APPLICANT: Carptén, John
APPLICANT: Trent, Jeffrey
APPLICANT: Trent, Jeffrey
APPLICANT: Marcelino, Jose
APPLICANT: Marcelino, Jose
TITLE OF INVENTION: Novel Methods and Reagents for the Treatment of Osteoarthritis
FILE REFERENCE: Case-06212
CURRENT APPLICATION NUMBER: US/09/802,207
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 09/619,175
PRIOR APPLICATION NUMBER: 09/619,338
PRIOR APPLICATION NUMBER: 60/145,328
   CURRENT APPLICATION NUMBER: US/10/038,694
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,920
PRIOR FILING DATE: 2000-12-29
  APPLICANT: Warman, Matthew
APPLICANT: Carpten, John
  APPLICANT: Su, Jui-Lan
TITLE OF INVENTION: SUPERFICIAL ZONE PROTEIN AND METHODS
TITLE OF INVENTION: MAKING AND USING SAME
FILE REFERENCE: 07083.0008U5
   APPLICANT:
   LENGTH: 538
TYPE: PRT
ORGANISM: Artificial Sequence
   INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
   OTHER INFORMATION: Description of Artificial Sequence; note OTHER INFORMATION: synthetic construct
  FEATURE:
  Local Similarity es 6; Conserv
  MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
   305 WMLSPFS 311
  230 WMLSPFS 236
  1 WMLSAFS 7
   1 WMLSAFS 7
  LENGTH: 463 amino acids TYPE: amino acid
  Hutchins, Jeff T.
Kuettner, Klaus E.
Schmid, Thomas M.
   TOPOLOGY: linear
   Schmid, Thomas M.
Schumacher, Barbara L.
   Conservative
  Conservative
  Eric
   85.7%;
  86.8%;
85.7%;
   0
  0; Mismatches
   Score 33;
Pred. No. 6
   Score 33; DB 4;
Pred. No. 6.9e+02;
0; Mismatches 1
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  DB 6;
  1; Indels
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  Length 463;
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  0,
   Gaps
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  0
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; LENGTH: 792
; TYPE: PRT
; ORGANISM: Homo sapiens
ERATURE:
; NAME/KEY: NON CONS
; LOCATION: (267)...(268)
; NAME/KEY: NON CONS
; LOCATION: (321)...(322)
US-09-802-207-27
  RESULT 26
US-10-425-115-337015
  문
   S
   RESULT 27
US-10-124-557-44
   밁
  Ş
   US-10-425-115-337015
  Sequence 44, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
   NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 337015
  NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version
SEQ ID NO 27
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  Query Match
Best Local (
   GENERAL INFORMATION:
  Sequence 337015, Application US/10425115
Publication No. US20040214272A1
   Matches
   Best
   Query Match
  APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
   CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
  NAME/KEY: unsure
LOCATION: (1)..(1046)
OTHER INFORMATION: unsure at all Xaa locations
   TYPE: PRT
ORGANISM: Zea mays
  OTHER INFORMATION: Clone ID: MRT4577_70527C.1.pep
   FEATURE:
  ENGTH: 1046
  Local Similarity 71.
   Match 86.8%; Local Similarity 85.7%; les 6; Conservative
                            TITLE OF INVENTION: Megakaryocyte
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
  APPLICANT: Turner, Katherine
   890 WLISAFS 896
  559 WMLSPFS 565
  1 WMLSAFS 7
   1 WMLSAFS
 STREET:
ADDRESSEE: Genetics Institute, Inc
STREET: 87 CambridgePark Drive
   Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
   Clark, Stephen C.
   7
   86.8%;
  3.0
   0;
   Score 33; DB 3;
Pred. No. 9.7e+02;
  Score 33; DB 4;
Pred. No. 1.2e+03;
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  Length 792;
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RESULT 28
US-11-169-232-44
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  á
  US-10-124-557-44
  Sequence 44, Application US/11169232 Publication No. US20060025570A1 GENERAL INFORMATION:
   Best Local Similarity
Matches 6; Conserv
  Query Match
  NAME: CSETT, LHAND
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-5851
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/11/169,232
   TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
   ATTORNEY/AGENT INFORMATION:
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
  1037 WMLSPFS 1043
   APPLICANT: Turner, Katherine
Clark, Stephen C.
  1 WMLSAFS 7
  STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
   APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991 APPLICATION NUMBER: US 07/546,114 FILING DATE: 29-UN-1990 APPLICATION NUMBER: US 07/457,196 FILING DATE: 29-DEC-1989
   COUNTRY: U.S.A.
ZIP: 02140
  APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002
  STATE: Massachusetts COUNTRY: U.S.A.
  TYPE: amino acid
   APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989
  ADDRESSEE: Genetics Institute,
   ENGTH: 1270 amino acids
   Conservative
   Hewick, Rodney M. Gesner, Thomas G.
   Jacobs,
  86.8%;
  Kenneth
   0
   Score 33; DB 4; Pred. No. 1.5e+03; 0; Mismatches 1
  Inc.
  Version #1.25
  Length 1270;
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   Gaps
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US-10-124-557-42
Sequence 42, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
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  US-11-169-232-44
   Matches
  Query Match
Best Local Similarity
   INFORMATION FOR SEQ ID NO: 44: SEQUENCE CHARACTERISTICS:
  APPLICATION NUMBER: US 07/643,502
APILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/457,196
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATECHTIN Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-App-2002
CLASSIFICATION: Unknown>
   TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
   FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
  TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
  APPLICANT: Turner, Katherine
Clark, Stephen C.
   1037 WMLSPFS 1043
  TELEPHONE: (617)876-1170
   1 WMLSAFS 7
   6;
  ZIP:
   STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusette
COUNTRY: U.S.A.
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
  REFERENCE/DOCKET NUMBER: GI
  APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002
  TYPE: amino acid
   NAME: Cserr,
  LENGTH: 1270 amino acids
   TELEFAX: (617)876-5851
   Conservative
  02140
   Hewick, Rodney M. Gesner, Thomas G.
  86.8%;
85.7%;
   Luann
   Kenneth
  <Unknown>
   0; Mismatches
  Score 33; DB 6;
Pred. No. 1.5e+03;
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  Version #1.25
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   Gaps
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RESULT 30
US-11-169-232-42
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   Ś
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Publication No.
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  Query Match
  Best
  GENERAL INFORMATION:
   TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 42:
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
FILING DATE: 29-DEC-1989
   y Match 86.8%;
Local Similarity 85.7%;
nes 6; Conservative
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
   REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
  APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989 ATTORNEY/AGENT INFORMATION:
  SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/11/169,232
FILING DATE: 28-Jun-2005
   1078 WMLSPFS 1084
   SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acids
                                     TELECOMMUNICATION INFORMATION:
  ATTORNEY/AGENT INFORMATION:
  CORRESPONDENCE ADDRESS:
   TITLE OF INVENTION: Megakaryocyte Stimulating NUMBER OF SEQUENCES: 143
  APPLICANT: Turner, Katherine
Clark, Stephen C.
   1 WMLSAFS
  NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
  STATE: Massachusetts COUNTRY: U.S.A.
  CITY: Cambridge
  STREET: 87 CambridgePark Drive
  NAME: Cserr,
  APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989
   TELEPHONE: (617)876-1170
  Application US/11169232
No. US20060025570A1
                 CELEPHONE:
   DDRESSEE:
   Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
E: (617)876-1170
(617)876-5851
  Genetics Institute,
  Luann
   Score 33; DB 4; Pred. No. 1.5e+03; 0; Mismatches 1
  42:
  Length 1311;
  Indels
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  Gaps
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LENGTH: 1313 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-10-124-557-142
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US-10-124-557-142
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  ş
  US-11-169-232-42
  Sequence 142, Applicat:
Publication No. US2002
GENERAL INFORMATION:
APPLICANT: Turn
   Matches
  Query Match
Best Local Similarity
Query Match
Best Local Similarity
   INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 1311 amino acids
   REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION: IMFORMATION:
TELEPHONE: (617)876-1170
TELEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
  APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
   Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
   TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 42:
   1078 WMLSPFS 1084
  COMPUTER READABLE FORM:
  1 WMLSAFS 7
   6
   STATE: Massachusetts
  ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
  TYPE: amino acid
   COUNTRY: U.S.A.
  CITY: Cambridge
   REGISTRATION NUMBER: 31,822
   NAME: Cserr,
   Application US/10124557

o. US20020137894A1
   Conservative
  Turner, Katherine
   Clark, Stephen C.
   86.8%;
86.8%;
85.7%;
   Luann
   0;
   Score 33; DB 6;
Pred. No. 1.5e+03;
Score 33; DB 4; Length 1313; Pred. No. 1.5e+03;
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  Length 1311;
   Indels
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   Gaps
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-11-169-232-142
   밁
   ş
밁
   RESULT 32
US-11-169-232-142
                              Š
  Sequence 142, Application US/11169232
Publication No. US20060025570A1
  Matches
   Matches
   Query Match
  GENERAL INFORMATION:
   INFORMATION FOR SEQ ID NO: 142:
   Local Similarity
mes 6; Conserv
  APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
  TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
1080 WMLSPFS 1086
   PRIOR APPLICATION DATA:
   CURRENT APPLICATION DATA:
   1080 WMLSPFS 1086
  SEQUENCE CHARACTERISTICS:
   CORRESPONDENCE ADDRESS:
  TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
   APPLICANT:
  1 WMLSAFS 7
                                   1 WMLSAFS 7
  6
  APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
   NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
  APPLICATION NUMBER: US/11/169,232 FILING DATE: 28-Jun-2005 CLASSIFICATION: <Unknown>
  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
   CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
  ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
   LENGTH: 1313 amino acids
  Conservative
   Conservative
   Turner, Katherine
Clark, Stephen C.
  Jacobs, Kenneth
  Hewick, Rodney M.
Gesner, Thomas G.
  86.8%;
  0;
   0
  Score 33; DB 6;
Pred. No. 1.5e+03
   Mismatches
  Mismatches
   5190
  .5e+03;
  ۲.
   Length 1313;
   Indels
  Indels
  0
   0
  Gaps
  0
   0
```

RESULT 33 US-10-124-557-50

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RESULT 34
US-11-169-232-50
   밁
  Ś
   US-10-124-557-50
  Sequence 50, Application US/11169232 Publication No. US20060025570A1 GENERAL INFORMATION:
   Matches
  Query Match
Best Local :
  Sequence 50, Application US/10124557 Publication No. US20020137894A1 GENERAL INFORMATION:
  INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/124,557

FILING DATE: 16-Apr-2002

CLASSIFICATION EATH.

APPLICATION **CURROWN**

PRIOR APPLICATION **CURROWN**

PRIOR APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 19-JUN-1990

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

APPLICATION UNBER: US 07/390,901

FILING DATE: 08-AUG-1989

APPLICATION UNBER: US 07/390,901

FILING DATE: 08-AUG-1989

APPLICATION UNBER: US 07/390,901
   Match 86.8%; Local Similarity 85.7%;
   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
  REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   1081 WMLSPFS 1087
   Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                           TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
   APPLICANT:
  CORRESPONDENCE ADDRESS:
  APPLICANT: Turner, Katherine
Clark, Stephen C.
         CORRESPONDENCE ADDRESS
   1 WMLSAFS 7
   STATE: Massachusetts COUNTRY: U.S.A.
  TYPE: amino acid
  NAME: Cserr,
   CITY: Cambridge
  STREET: 87 CambridgePark Drive
   LENGTH: 1314 amino acids
   ADDRESSEE: Genetics Institute,
   Conservative
   Turner, Katherine
Clark, Stephen C.
   Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
   Score 33; DB 4;
Pred. No. 1.5e+03;
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  Length 1314;
  1; Indels
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  Gaps
  ٥,
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US-10-124-557-46
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   ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 50: US-11-169-232-50
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  Sequence 46, Application US/10124557 Publication No. US20020137894A1 GENERAL INFORMATION:
   Matches
  Query Match
Best Local :
  TELEFAX: (617)876-5851 INFORMATION FOR SEQ ID NO: 50:
   PRIOR APPLICATION: «Unknown»

APPLICATION DATA:

APPLICATION NUMBER: US/10/124,557

FILING DATE: 16-Apr-2002

APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-JUN-1990

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

APPLICATION NUMBER: US 07/390,901
   Local Similarity es 6; Conserv
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
   TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
   1081 WMLSPFS 1087
   SEQUENCE CHARACTERISTICS:
  REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
  COMPUTER READABLE FORM:
  CORRESPONDENCE ADDRESS:
  APPLICANT: Turner, Katherine
Clark, Stephen C.
   1 WMLSAFS
   ZIP:
  CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
   ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
   LENGTH: 1314 amino acids TYPE: amino acid
  NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
החייים/חסכKET NUMBER: GI 5190
   ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive CITY: Cambridge
  STATE: Massachusetts
  TOPOLOGY: linear
  MEDIUM TYPE: Floppy disk
   TELEPHONE: (617)876-1170
  COUNTRY: U.S.A.
   Conservative
   02140
   Hewick, Rodney M. Gesner, Thomas G.
   Jacobs, Kenneth
   7
  86.8%;
   0
  Score 33; DB 6;
Pred. No. 1.5e+03;
   Mismatches
  Inc
  Inc.
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Length 1314; Indels

0

Gaps

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  뭉
  RESULT 36
US-10-124-557-60
  US-10-124-557-46
  Sequence 60, Application US/1011
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Kathen
  Matches
  Best Local Similarity
  Query Match
   INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 amino acids
  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
   REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
   ATTORNEY/AGENT INFORMATION:
   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-App-2002
CLASSIFICATION: <Unknown>
  1087 WMLSPFS 1093
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
   PRIOR APPLICATION DATA:
  CORRESPONDENCE ADDRESS:
  TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
   APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
  1 WMLSAFS 7
  6
   NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
   CLASSIFICATION: < Unknown>
   FILING DATE: 16-Apr-2002
   APPLICATION NUMBER: US/10/124,557
  CITY: Cambridge
STATE: Massachusetts
  ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
  TYPE: amino acid
   COUNTRY: U.S.A.
   ADDRESSEE:
  Application US/10124557
  Conservative
  Turner, Katherine
Clark, Stephen C.
  Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
  86.8%;
  0; Mismatches
  Score 33; DB 4;
Pred. No. 1.5e+03;
  1; Indels
  Length 1320;
  0;
  Gaps
  0
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밁
   ; ORGANISM: Homo sapiens US-10-717-665-58
  Ş
   RESULT 38
US-11-169-232-46
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  US-10-717-665-58
   RESULT 37
  US-10-124-557-60
   Sequence 58, Application US/10717665
Publication No. US20050106579A1
GENERAL INFORMATION:
APPLICANT: Oridene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REFERENCE: 1U 103 R1
CURRENT APPLICATION NUMBER: US/10/717,665
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US/10/164,595
PRIOR FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
  Sequence 46, Application US/11169232 Publication No. US20060025570A1 GENERAL INFORMATION:
  SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
LENGTH: 1320
  Matches
   Query Match
Best Local (
   Matches
   Query Match
  TELEFAX: (617)876-58
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
   TYPE: PRT
   86.8%;
Local Similarity 85.7%;
les 6; Conservative
   Local Similarity nes 6; Conserv
   APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
   MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
  REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION
  1087 WMLSPFS 1093
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
   1087 WMLSPFS 1093
  TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
  APPLICANT: Turner, Katherine
Clark, Stephen C.
  1 WMLSAFS 7
   1 WMLSAFS 7
   NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REGISTRATION NUMBER: GI
   TYPE: amino acid TOPOLOGY: linear
   LENGTH: 1320 amino acids
  TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
   Conservative
   Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
  86.8%;
   0
  0;
   Score 33; DB 5; I
Pred. No. 1.5e+03;
0; Mismatches 1,
  Score 33; DB 4; ]
Pred. No. 1.5e+03;
0; Mismatches 1
   60:
   5190
                    Inc
  Length 1320;
   Length 1320;
  Indels
   Indels
  0;
   0
  Gaps
   Gaps
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   0,
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US-11-169-232-60
; Sequence 60, Applicatio
; Publication No. US20060
; Publication INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Turne
  TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-11-169-232-46
  Ş
   RESULT 39
   밁
  Matches
  Query Match
Best Local Similarity
  INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
ZIP: 0214v

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

ROFTWARE: PatentIn Release #1.0, Ve
  APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: CUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/457,901
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
   TELEFAX: (617)876-5851
  Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
   ATTORNEY/AGENT INFORMATION:
   1087 WMLSPFS 1093
  CORRESPONDENCE ADDRESS:
  1 WMLSAFS 7
  6,
   NAME: Cserr, Luann
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
   CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
   CITY: Cambridge
STATE: Massachusetts
  ADDRESSEE: Genetics Institute, Inc
STREET: 87 CambridgePark Drive
  COUNTRY: U.S.A.
   TYPE: amino acid
   ENGTH: 1320 amino acids
  Application US/11169232
  Conservative
   US20060025570A1
   Turner, Katherine
Clark, Stephen C.
  86.8%;
85.7%;
  Katherine
  0,
  Score 33; DB 6; Length 1320; Pred. No. 1.5e+03;
  Mismatches
   5190
   46:
                               Version #1.25
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  Gaps
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  RESULT 40
US-10-124-557-48
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  US-11-169-232-60
  Sequence 48, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
  Matches
  Query Match
Best Local
   TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION ACUKNOWN>
PRIOR APPLICATION NUMBER: US 07/643,502
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
  PRIOR APPLICATION DATA:

PRIOR APPLICATION UNMBER: US/10/124,557

FILING DATE: 16-Apr-2002

APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-UN-1990

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

FILING DATE: 29-DEC-1989
  Local Similarity 85.
   APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
   TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
   NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
   TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
  1087 WMLSPFS 1093
  CURRENT APPLICATION DATA:
   CORRESPONDENCE ADDRESS:
   APPLICANT: Turner, Katherine
Clark, Stephen C.
   1 WMLSAFS 7
  STATE: Massachusetts COUNTRY: U.S.A.
   ADDRESSEE: Genetics Institute, Inc
STREET: 87 CambridgePark Drive
CITY: Cambridge
   CLASSIFICATION:
   APPLICATION NUMBER: US/11/169,232 FILING DATE: 28-Jun-2005
  LENGTH: 1320 amino acids
  Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
  86.8%;
   <Unknown>
  0,
  Score 33; DB 6; 1
Pred. No. 1.5e+03;
0; Mismatches 1
  5190
  Length 1320;
  Indels
  0
  Gaps
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US-11-169-232-48
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  US-10-124-557-48
  Sequence 48, Application US/111.
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Kathe
   Matches
  Query Match
   INFORMATION FOR SEQ ID NO: 48: SEQUENCE CHARACTERISTICS:
   APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
   Match 86.8%;
Local Similarity 85.7%;
   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
  ZIP: 02140
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
   NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
  APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
   Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
   1121 WMLSPFS 1127
   ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
  CORRESPONDENCE ADDRESS:
  1 WMLSAFS 7
   6
   APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
   CITY: Cambridge
STATE: Massachusetts
                 REGISTRATION NUMBER: 31,822
  TYPE: amino acid
  TELEFAX: (617)876-5851
  COUNTRY: U.S.A.
  STREET: 87 CambridgePark Drive
  NAME:
  ADDRESSEE: Genetics Institute, Inc
   LENGTH: 1354 amino acids
   TELEPHONE: (617)876-1170
   Application US/11169232
   Conservative
  Turner, Katherine
  Cserr,
   Jacobs, Kenneth
   Clark, Stephen C.
  Luann
   °:
   Score 33; DB 4;
Pred. No. 1.6e+03;
   Mismatches
  Length 1354;
   1; Indels
   0;
   Gaps
   0;
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Query Match
Best Local Similarity
Matches 6; ConBerva
   RESULT 42
US-10-124-557-40
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   US-11-169-232-48
US-10-124-557-40
  Sequence 40, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
  INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
  INFORMATION FOR SEQ ID NO: 40: SEQUENCE CHARACTERISTICS:
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FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
   SOFTWARE: PatentIn Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
  MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 48:
   REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (617)876-1170
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetic
  1121 WMLSPFS 1127
   TITLE OF INVENTION: Megakaryocyte Stimulating Factors
  APPLICANT: Turner, Katherine
Clark, Stephen C.
  NUMBER OF SEQUENCES: 143
  1 WMLSAFS 7
  TELEPHONE:
  NAME: Cserr, Luann
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
  STATE: Massachusetts
  TOPOLOGY: linear
   TYPE: amino acid
   TYPE: amino acid
   COUNTRY: U.S.A.
   CITY: Cambridge
   STREET: 87 CambridgePark Drive
  LENGTH: 1354 amino acids
  TELEFAX:
   TELEPHONE: (617)876-1170
  LENGTH: 1361 amino acids
  Conservative
  Hewick, Rodney M. Gesner, Thomas G.
  (617)876-5851
  (617)876-5851
   86.8%;
  Genetics Institute,
  Kenneth
  Mismatches
   Score 33; DB 6;
Pred. No. 1.6e+03;
  Inc.
  Version #1.25
  1; Indels
  Length 1354;
  <u>,</u>
  Gaps
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RESULT 43
US-11-169-232-40
; Sequence 40, Application
; Publication No. US200600
; Publication INFORMATION:
  밁
  S
 맑
                                 Ś
  US-11-169-232-40
  Query Match
Best Local S
Matches 6
  Matches
  Query Match
Best Local Similarity
   INFORMATION FOR SEQ ID NO: 40: SEQUENCE CHARACTERISTICS:
  Local Similarity
les 6; Conserv
   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE

COMPATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
  Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
   TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
  REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
  APPLICANT: Turner, Katherine
Clark, Stephen C.
  1128 WMLSPFS 1134
1128 WMLSPFS 1134
   ATTORNEY/AGENT INFORMATION:
  PRIOR APPLICATION DATA:
  CORRESPONDENCE ADDRESS:
  APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
  1 WMLSAFS 7
   6; Conservative
                                     WMLSAFS 7
   NAME: CBerr, Luann
NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
   APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
   CITY: Cambridge
STATE: Massachusetts
   TYPE: amino acid
   ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
   COUNTRY: U.S.A.
  LENGTH: 1361 amino acids
  Application US/11169232
  TELEFAX: (617)876-5851
   TELEPHONE:
  86.8%;
nilarity 85.7%;
Conservative
  86.8%;
   (617)876-1170
   Kenneth
   0
  Score 33; DB 4; Length 1361; Pred. No. 1.6e+03; 0; Mismatches 1; Indels
  Score 33; DB 6;
Pred. No. 1.6e+03;
   Mismatches
   5190
   40:
  Inc
  Version #1.25
   1; Indels
  Length 1361;
  0,
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   Gaps
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RESULT 44
US-10-124-557-52
; Sequence 52, Application US/10124557
; Publication No. US20020137894A1
; GENERAL INFORMATION:
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US-11-169-232-52
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   US-10-124-557-52
   Sequence 52, Appublication No.
  Matches
  Query Match
Best Local Similarity
   GENERAL INFORMATION:
   INFORMATION FOR SEQ ID NO: 52:
  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-JUN-1990

APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOMBER: US/10/124,557
FILING DATE: 16-Apr-2002
              APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
   NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
   1130 WMLSPFS 1136
   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
   NAME: CGETT, LUANN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
  ATTORNEY/AGENT INFORMATION:
TITLE OF
  SEQUENCE CHARACTERISTICS:
   TITLE OF INVENTION: Megakaryocyte Stimulating Factors
  APPLICANT: Turner, Katherine
Clark, Stephen C.
   1 WMLSAFS
  6;
   STATE: Massachusetts COUNTRY: U.S.A.
  TYPE: amino acid
   CLASSIFICATION: <Unknown>
  CITY: Cambridge
   TELEFAX:
   Application US/11169232
  ENGTH: 1363 amino acids
   TELEPHONE:
  ADDRESSEE:
  Conservative
INVENTION:
   US20060025570A1
   Hewick, Rodney M. Gesner, Thomas G.
  Jacobs, Kenneth
  87 CambridgePark Drive
   (617)876-5851
  Genetics Institute,
  86.8%;
85.7%;
   (617)876-1170
Megakaryocyte Stimulating Factors
  Score 33; DB 4; Leg
Pred. No. 1.6e+03;
  5190
  Inc.
  Length 1363;
  Indels
  0,
  Gaps
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  US-09-802-207-30
   RESULT 46
   US-11-169-232-52
   GENERAL INFORMATION:
   Sequence 30, Application US/09802207 Publication No. US20020086824A1
  Matches
   Query Match
Best Local Similarity
  CURRENT APPLICATION NUMBER: US/09/802,207
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: 09/619,175
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 60/145,328
PRIOR FILING DATE: 1999-07-23
  APPLICANT: Warman, Matthew
APPLICANT: Carpten, John
APPLICANT: Trent, Jeffrey
APPLICANT: Trent, Jose
APPLICANT: Marcelino, Jose
TITLE OF INVENTION: Novel Methods and Reagents for the Treatment of Osteoarthritis
FILE REFERENCE: Case-06212
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
  INFORMATION FOR SEQ ID NO: 52:
  APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 16-ALN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DBC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION:
  1130 WMLSPFS 1136
  SEQUENCE CHARACTERISTICS:
  TELECOMMUNICATION INFORMATION:
  ATTORNEY/AGENT INFORMATION:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  CORRESPONDENCE ADDRESS:
   NUMBER OF SEQUENCES: 143
  1 WMLSAFS 7
   6;
  NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
   CITY: Cambridge
STATE: Massachusetts
  ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
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Publication No. US20040072741A1
GENERAL INFORMATION:
APPLICANT: Jay, Gregory D.
TITLE OF INVENTION: Tribonectin Po
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PRIOR FILING DATE: 1999-04-23
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OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1

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   APPLICANT: Turner, Katherine
Clark, Stephen C.
  TITLE OF INVENTION: Megakaryocyte Stimulating
  1 WMLSAFS 7
  1 WMLSAFS 7
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6; Conserva
   STATE: Massachusetts COUNTRY: U.S.A.
  ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
  CITY: Cambridge
CLASSIFICATION: <Unknown>
   OF SEQUENCES:
  Conservative
  Jacobs, Kenneth
   Hewick, Rodney M.
Gesner, Thomas G.
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TOPOLOGY: linear
MOLECULE TYPE: protein
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01/24,557

FILING DATE: 16-Apr-202
CLASSIFICATION UNMBER: US 07/643,502
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APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/457,196
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-UN-1990
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FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
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FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
  Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
  1171 WMLSPFS 1177
  TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
  CORRESPONDENCE ADDRESS:
   APPLICANT: Turner, Katherine Clark, Stephen C.
   PRIOR APPLICATION DATA:
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  NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
  STATE: Massachusetts COUNTRY: U.S.A.
  CITY: Cambridge
  TELEFAX: (617)876-5851
   STREET: 87 CambridgePark Drive
  LENGTH: 1404 amino acids
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  APPLICANT: Jay, Gregory D.
TITLE OF INVENTION: TRIBONECTINS
FILE REFERENCE: 21486-026
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25 65 55 55 55 55 55 55 55 55 55 55 55 55	25 65.8 25 65.8 25 65.8 65.8	25 65.8 8 65.8	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	25 65.8 25 65.8 25 65.8	25 65.8 25 65.8 25 65.8	25 65. 65. 65. 8 8	00000000000000000000000000000000000000	25 65. 65. 65. 8 8	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	25 65.8 25 65.8 25 65.8	25 65.8	25 5 65.8	25 65.8 65.8	255 65.	25 65.8 65.8	25 65.8 25 65.8
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S-11-221-332-12
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: National Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205YI-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
FRIOR APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
FRIOR APPLICATION NUMBER: JP 2002-203269
FRIOR APPLICATION NUMBER: JP 2002-383870
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FRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28641
FYPE: PRT
GRGANISM: Oryza sativa
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Sequence 28641, Application US/10449902
Publication No. US20060123505A1
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
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PRIOR FILING DATE: 2004-06-30
  PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOSTTWARE: Patentin Ver: 2.1
   CURRENT FILING DATE: 2005-06-30
   APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: UCCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
  FILE REFERENCE: 2750-1601PUS2
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US-11-354-310A-14

Sequence 14, Application US/11354310A
Publication No. US20060185037A1
GENERAL INFORMATION:
APPLICANT: Sticklen, Masomeh B
APPLICANT: Magbool, Shahina B

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  US-11-353-390A-14
  SOFTWARE: PatentIn version 3.3 SEQ ID NO 14
   GENERAL INFORMATION:
APPLICANT: Sticklen, Masomeh B
APPLICANT: Magbool, Shahina B
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APPLICANT: Dale, Bruce E
TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULASE WHICH
TITLE OF INVENTION: DEGRADE LIGNIN AND CELLULOSE TO FERMENTABLE SUGARS
  Sequence 14, Application US/11353390A
Publication No. US20060185036A1
   SOFTWARE: PatentIn version 3.3
SEQ ID NO 14
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CURRENT FILING DATE: 2006-04-06
PRIOR APPLICATION NUMBER: US 60/242,408
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 09/981,900
PRIOR PILING DATE: 2001-10-18
NUMBER OF SEQ ID NOS: 22
  PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 09/981,900
PRIOR FILING DATE: 2001-10-18
  APPLICANT: Sticklen, Masomeh B
APPLICANT: Magbool, Shahina B
APPLICANT: Dale, Bruce E
   FILE REFERENCE: MSU 4.1-806
CURRENT APPLICATION NUMBER: US/11/353,390A
CURRENT FILING DATE: 2006-02-14
CURRENT APPLICATION NUMBER: US 60/242,408
PRIOR APPLICATION NUMBER: US 60/242,408
   TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULASE TITLE OF INVENTION: DEGRADE LIGNIN AND CELLULOSE TO FERMENTABLE SUGARS FILE REFERENCE: MSU 4.1-814
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85.7%;
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Sequence 46157, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902
   PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
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  APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: 1910/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR PILING DATE: 2002-05-30
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CURRENT FILING DATE: 2006-02-14
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PRIOR FILING DATE: 2000-10-20
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PRIOR FILING DATE: 2001-10-18
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CURRENT FILLING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
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PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y10
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
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APPLICANT: Bio-oriented Technology Research Advancement
APPLICANT: The Institute of Physical and Chemical Research
APPLICANT: Foundation for Advancement of International S
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PRIOR FILING DATE: 2002-05-30
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LOCATION: (1)...(297)

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US-11-056-355B-79384
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US-10-449-902-44647
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US-10-953-349-38417
  Sequence 38417, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT PILING DATE: 2004-09-30
RUMBER OF SEQ ID NOS: 40252
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   APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
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CURRENT FILING DATE: 2005-02-14
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  APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
IITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
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TITLE OF INVENTION: Polypeptides Encoded Thereby
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306 WLLAAFT 312
   233 WLLIAFS
   230 WLLIAFS 236
   1 WMLSAFS
  1 WMLSAFS 7
   1 WMLSAFS 7
   4;
   Conservative
  Conservative
   239
   76.3%;
  76.3%;
57.1%;
  Score 29; DB 7;
Pred. No. 1.6e+02;
1; Mismatches 1
   Score 29; DB 7;
Pred. No. 1.7e+02;
3; Mismatches 0
   ID no. 12666048
   Length 334;
  Length 308;
  and Corresponding
   <u>,,</u>
  0
  Gaps
   Gaps
   0
  0
```

US-10-511-455-26

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밁
  ; ORGANISM: Homo sapiens US-10-511-455-26
   US-11-395-249-4
  PRIOR APPLICATION NUMBER: GB0207902.8
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: GB0207904.4
PRIOR TILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: GB0207900.2
PRIOR APPLICATION NUMBER: GB0207900.2
PRIOR APPLICATION NUMBER: GB0207901.0
PRIOR APPLICATION NUMBER: GB0227734.1
PRIOR APPLICATION NUMBER: GB0227734.1
   Sequence 26, Application US/10511455
Publication No. US20060088835A1
  GENERAL INFORMATION:
   Matches
   SEQ ID NO 26
  GENERAL INFORMATION:
  SEQ ID NO 4
  Sequence 4, Application US/11395249 Publication No. US20060177904A1
   APPLICANT:
   APPLICANT: Fechtel, Kim
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 00766,000103.6
CURRENT APPLICATION NUMBER: US/11/395,249
CURRENT FILING DATE: 2006-04-03
NUMBER OF SEQ ID NOS: 240
NUMBER OF SEQ ID NOS: 250
   APPLICANT:
   APPLICANT: Jacobs,
APPLICANT: McCoy,
APPLICANT: LaVall:
  NUMBER OF SEQ ID NOS: 94
   CURRENT APPLICATION NUMBER: US/10/511,455
CURRENT FILING DATE: 2004-10-05
PRIOR APPLICATION NUMBER: PCT/GB03/001543
PRIOR FILING DATE: 2003-04-07
  APPLICANT: Ewald, Henrik Lykke
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES
  APPLICANT: Pickard, Benjamin Simon APPLICANT: Blackwood, Douglas
   APPLICANT:
  FILE REFERENCE: 9013.63
   APPLICANT:
  APPLICANT:
  PRIOR FILING DATE: 2002-11-28
   APPLICANT:
  APPLICANT:
ORGANISM: Homo sapiens
   ENGTH:
                                      ENGTH: 335
   76.3%;
Local Similarity 83.3%;
es 5; Conservation
   1 WMLSAF 6
  PatentIn version 3.1
  WMLSIF 321
   Muir, Walter John
  Porteous, David
   Agostino, Michael J.
Steininger II, Robert J.
Spaulding, Vikki
Wong, Gordon G.
   Collins-Racie, Lisa
Evans, Cheryl
   McCoy, John M.
  Merberg, David
Treacy, Maurice
   ark, Hilary
   llie, Edward R.
   OLe
  Kenneth
   0; Mismatches
   Score 29; I
Pred. No. 1
   Þ
   DB 6;
1.7e+02;
   1; Indels
  Length 335;
   0
   Gaps
   0
```

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RESULT 18
US-10-93-349-33299
; Sequence 33299, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
   Query Match
Best Local Similarity
Theches 5; Conserve
   Query Match
Best Local Similarity
Matches 5; Conserve
   밁
   ; ORGANISM: Zea mays subsp. mays US-10-953-349-33299
  RESULT 17
US-11-056-355B-82529
   뫄
  US-11-056-355B-82529
   US-11-395-249-4
  APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 33299
LENGTH: 345
TYPE: PRT
   APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR OF SEQ ID NOS: 119966
SEQ ID NO 82529
LENGTH: 338
   Sequence 82529, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
   Matches
   Query Match
Best Local
  NAME/KEY: peptide
LOCATION: (1)..(338)
OTHER INFORMATION: Ceres Seq. ID no. 12666052
  TYPE: prt
  ORGANISM: Arabidopsis thaliana
  Local Similarity es 4; Conserv
   |:|:||:
310 WLLAAFT 316
   316 WMLSIF 321
270 WLLIAFS
   1 WMLSAFS 7
  1 WMLSAF 6
                                      1 WMLSAFS
   Conservative
  Conservative
  Conservative
 276
   76.3%;
83.3%;
   76.3%;
57.1%;
   76.3%;
71.4%;

    Mismatches

   3; Mismatches
  0; Mismatches
   Score 29; DB 6;
Pred. No. 1.8e+0
   Score 29; 1
Pred. No. 1
   Score 29; DB 7;
Pred. No. 1.7e+02;
   DB 7;
1.7e+02;
   .8e+02;
   Length 345;
  Length 338;
  Length 335;
  Indels
   0
  0
  0,
  Gaps
  Gaps
  0
   0
```

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밁
   á
  US-10-449-902-30511
  RESULT 21
   밁
  5
  US-11-056-355B-79382
  RESULT 20
   ; ORGANISM: Zea mays subsp. mays US-10-953-349-38416
  US-10-953-349-38416
  US-11-056-355B-79382
   CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 38416
   GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
  Sequence 30511, Application US/10449902 Publication No. US20060123505A1 GENERAL INFORMATION:
   Sequence 38416, Application US/10953349 Publication No. US20060107345A1
  Matches
  SEQ ID NO 79382
  GENERAL INFORMATION:
   Sequence 79382, Application US/11056355B Publication No. US20060150283A1
   Matches
   Query Match
   Query Match
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Paylical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
   PEATURE:
NAME/KEY: peptide
LOCATION: (1)..(351)
OTHER INFORMATION: Ce
   PRIOR APPLICATION NUMBER: 60/544,190 PRIOR FILING DATE: 2004-02-13 NUMBER OF SEQ ID NOS: 119966
   TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 2750-1590PUS2 CURRENT APPLICATION NUMBER: US/11/056,355B CURRENT FILING DATE: 2005-02-14
   APPLICANT: Brover, Vyacheslav APPLICANT: Alexandrov, Nickolai
  LENGTH: 351
TYPE: prt
ORGANISM: Arabidopsis thaliana
  TYPE: PRT
   ENGTH: 345
  Match 76.3%;
Local Similarity 71.4%;
   Local Similarity
   273
   270 WLLIAFS 276
   1 WMLSAFS 7
  1 WMLSAFS 7
   5; Conservative
  WLLIAFS
  Conservative
   279
   Ceres Seq. ID no. 12651073
   76.3%;
   Score 29; DB 7;
Pred. No. 1.8e+02;
   1; Mismatches
  Score 29; DB 6;
Pred. No. 1.8e+02;
  Mismatches
   1; Indels
   Length 351;
   Length 345;
  0;
  Gaps
   Gaps
  0
   0
```

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밁
  밁
  ; ORGANISM: Oryza sativa 
US-10-449-902-49957
   ş
  ; ORGANISM: Oryza sativa
US-10-449-902-30511
   ş
   US-10-449-902-49957
  US-10-953-349-32815
   RESULT 23
Sequence 32815, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3

SEQ ID NO 32815
LENGTH: 355
TYPE: PRT
  GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29
  PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 49957
   Sequence 49957, Application US/10449902
Publication No. US20060123505A1
  SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30511
LENGTH: 354
TYPE: PRT
   Matches
   Matches
  Query Match
   Best
   Query Match
   PRIOR APPLICATION NUMBER: JP 2002-383870 PRIOR FILING DATE: 2002-12-11 NUMBER OF SEQ ID NOS: 56791
   CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILLING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
  TYPE: PRT
  LENGTH:
   Local Similarity tes 5; Conserv
   Local Similarity
Les 5; Conserv
  279 WLLIAFS 285
   279 WLLIAFS 285
  354
  1 WMLSAFS 7
   1 WMLSAFS 7
   Conservative
   Conservative
  76.3%;
71.4%;
   76.3%;
71.4%;

    Mismatches

  Score 29; DB 6;
Pred. No. 1.8e+02;
   Score 29; DB 6;
Pred. No. 1.8e+02;
1; Mismatches 1
  Length 354;
   Length 354;
   Indels
  Indels
   0,
   0.
   Gaps
   Gaps
   0
  0
```

```
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
FITILE OF INVENTION: Sequence Determined DNA Fragments and
FITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590FUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR PILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 11231
LENGTH: 355
  ; ORGANIŚM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)...(355)
; OTHER INFORMATION: Ceres Seq.
US-11-056-355B-17746
   RESULT 25
US-11-056-355B-17746
   밁
  Ś
   US-11-056-355B-11231
   RESULT 24
  밁
  Ś
   ; ORGANISM: Zea mays subsp. mays US-10-953-349-32815
  US-11-056-355B-11231
   Sequence 11231, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
   TITLE OF INVENTION: Sequence Determined DNA Fragments
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 17746
LENGTH: 355
  GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
   Sequence 17746, Application US/11056355B Publication No. US20060150283A1
  Matches
   Query Match
Query Match
Best Local
  Matches
  Query Match
   FEATURE:
NAME/KEY: peptide
LOCATION: (1)...(355)
OTHER INFORMATION: Ceres Seq. ID no.
   TYPE: prt
   TYPE: prt
ORGANISM: Zea mays
   Local Similarity 71.
  ocal
  280
   280 WLLIAFS 286
  1 WMLSAFS 7
  1 WMLSAFS 7
  Similarity 5; Conserv
Similarity
  WLLIAFS 286
  Conservative
   subsp.
  76.3%;
71.4%;
   76.3%;
71.4%;
76.3%;
71.4%;
  Seq. ID no. 13492044
   mays
  Score 29; DB
Pred. No. 1.8e
1; Mismatches
  1:
  Score 29; DB 7;
Pred. No. 1.8e+02;
Score
Pred.
  Mismatches
29;
  13492044
   DB 6; 1
DB 7;
1.8e+02;
  1; Indels
   Length 355;
   Length 355;
                Length 355;
  and
  and Corresponding
  Corresponding
   0,
  0
  Gaps
  0
  0
```

```
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCOMDED THERBY
FILE REPERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 33298
LENGTH: 357
   US-11-30-403-6594
US-11-310-403-6594
; Sequence 6594, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
   Ś
  Query Match
Best Local Similarity
Thehes 5; Conserve
  밁
  S
   ; TYPE: PRT; ORGANISM: Zea mays subsp. US-10-953-349-33298
   US-10-953-349-38415
  RESULT 27
  US-10-953-349-33298
  Sequence 33298, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
  CURRENT FILING DATE: 2004-09-
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 38415
LENGTH: 357
  Sequence 38415, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
  Matches
   Matches
  Query Match
Best Local
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38 8-21 (53629) B
CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
   APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
   FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
  TYPE: PRT ORGANISM: Zea mays subsp. mays
  280 WLLIAFS 286
   282 WLLIAFS
   282 WLLIAFS 288
   1 WMLSAFS
   1 WMLSAFS
   Similarity 5; Conserv
  ა
•
  WMLSAFS
   Conservative
   Conservative
  Conservative
   J
   288
  2004-09-30
  76.3%;
71.4%;
  76.3%;
71.4%;
  mays
  ۳.
  Score 29; DB 6;
Pred. No. 1.8e+02;
  Score 29; DB 6;
Pred. No. 1.8e+02;
   Mismatches
   Mismatches
  Mismatches
  DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
   DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
  1;
   Length 357;
   Length 357;
  Indels
   0
  0
   0;
   Gaps
   0
   0
  0
```

```
Query Match
Best Local Similarity
Thehes 5; Conserv
   5
  밁
  Ś
   ; ORGANISM: Magnaporthe grisea US-11-330-403-6594
  RESULT 30
US-10-953-349-33297
   멍
   ; ORGANISM: Oryza sativa 
US-10-449-902-38671
  ; ORGANISM: Zea mays subsp. mays US-10-953-349-33297
  US-10-449-902-38671
  APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 33297
  Sequence 33297, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
   NUMBER OF SEQ
SEQ ID NO 6594
   Matches
   Query Match
   SEQ ID NO 38671
  GENERAL INFORMATION:
  Sequence 38671, Application US/10449902 Publication No. US20060123505A1
  Query Match
        Matches
  APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LERGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-AD2051-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
   PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
   PRIOR APPLICATION NUMBER: JP 2002-203269 PRIOR FILING DATE: 2002-05-30
   SOFTWARE: Patentin Ver.
   TYPE: PRT
   TYPE: PRT
   LENGTH: 388
  LENGTH: 417
   ENGTH:
y watch 76.3%; Score 29; DB 6; Local Similarity 71.4%; Pred. No. 2.1e+02; hes 5; Conservative 1. Micmoralia
   76.3%;
Local Similarity 71.4%;
tes 5; Conservation
   311 WLLIAFS 317
  43 WMLSLF 48
   367
   1 WMLSAFS 7
  1 WMLSAF 6
  Conservative
   ID NOS: 19250
  76.3%;
   70-15
   ۲.
  ٥,
  Score 29; DB 7;
Pred. No. 1.9e+02;
0; Mismatches 1
   Score 29; DB 6;
Pred. No. 2e+02;
   Mismatches
   DB 6;
  Length 417;
   Length 367;
   1; Indels
   Length 388;
  Indels
        Indels
  0,
   0
      ٥,
   Gaps
  Gaps
      Gaps
  0
      0;
   0
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   S
US-11-056-355B-17744
Sequence 17744, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
   Ś
  멍
  ; ORGANISM: Zea mays subsp. mays US-10-953-349-32813
  밁
   밁
   US-11-056-355B-11229
  US-11-056-355B-11229
  RESULT 32
  US-10-953-349-32813
   RESULT 31
  RESULT 33
   Sequence 32813, Application US/10953349
publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
  CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 32813
LENGTH: 418
TYPE: PRT
  CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 11229
LENGTH: 418
   Sequence 11229, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
   Query Match
Best Local
  Query Match
Best Local
   Matches
  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 2750-1590PUS2
  APPLICANT: Brover, Vyacheslav APPLICANT: Alexandrov, Nicko
   TYPE: prt
ORGANISM: Zea mays subsp.
FEATURE:
  LOCATION: (1)..(418)
OTHER INFORMATION: C
   NAME/KEY: peptide
LOCATION: (1)..(4
   Local
  342 WLLIAFS 348
  343 WLLIAFS 349
   343 WLLIAFS 349
   1 WMLSAFS 7
  l Similarity
5; Conserv
  1 WMLSAFS 7
  1 WMLSAFS 7
   Similarity 5; Conserv
  Alexandrov, Nickolai
   Conservative
  Conservative
  Ceres Seq.
   76.3%;
71.4%;
  76.3%;
   Score 29;
Pred. No.
  ID no. 13492042
   Score 29; DB 7;
Pred. No. 2.1e+02;
1; Mismatches 1
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   2.1e+02;
   DB 7;
  DB 6;
   Length 418;
  Length 418;
  0;
   0
  Gaps
   Gaps
  0
   0
```

Vyacheslav

```
RESULT 35
US-11-056-355B-82528
  B
  S
   ; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)...(437)
; OTHER INFORMATION: Ceres Seq. ID no. 12666047
US-11-056-355B-82524
  밁
   Ś
  US-11-056-355B-82524
   US-11-056-355B-17744
   APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT FILING DATE: 2005-02-14
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 82524
LENGTH: 437
  Sequence 82528, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
  Sequence 82524, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
   CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 17744
  Matches
  Query Match
Best Local
  Matches
  Query Match
Best Local
                APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
   APPLICANT: Brover, Vyacheslav APPLICANT: Alexandrov, Nicko
  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 2750-1590FUS2
  CURRENT APPLICATION
  NAME/KEY: peptide
LOCATION: (1)..(418)
OTHER INFORMATION: C
  TYPE: prt
ORGANISM: Arabidopsis thaliana
  TYPE: prt
ORGANISM: Zea mays subsp. mays
   FEATURE:
   ENGTH: 418
  343 WLLIAFS 349
  409 WLLAAFT 415
   1 WMLSAFS 7
  Similarity 5; Conserv
  4.
  Similarity
   WMLSAFS 7
  Alexandrov, Nickolai
   Conservative
  Conservative
  NUMBER:
  Ceres Seq. ID no.
  76.3%;
57.1%;
  76.3%;
71.4%;
US/11/056,355B
  Score 29; DB Pred. No. 2.1e
1; Mismatches
  Score 29; DB 7;
Pred. No. 2.2e+02
  Mismatches
  13492042
  DB 7;
2.1e+02;
  Length 437;
  Length 418;
  Indels
  Indels
   0,
  0
   0;
  0
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  ; ORGANISM: Triticum aestivum US-10-953-349-31757
  밁
  Ś
   US-11-056-3558-66755, Application US/11056355B; Sequence 66755, Application US/11056355B; Publication No. US20060150283A1; GENERAL INFORMATION:
  RESULT 37
   US-10-953-349-31757
   RESULT 36
  US-11-056-355B-82528
   APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments of TITLE OF INVENTION: Sequence Determined DNA Fragments of TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT FILLING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR PILLING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 66755
  FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31757
LENGTH: 495
  Sequence 31757, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
  SEQ ID NO 82528
LENGTH: 438
   Matches
  Matches
  Query Match
  Best
   Query Match
   Best
  CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
  APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
  APPLICANT: Brover, Vyacheslav APPLICANT: Alexandrov, Nickol
  TYPE: prt
ORGANISM: Arabidopsis thaliana
   TYPE: prt
ORGANISM: Triticum aestivum
   TYPE: PRT
   NAME/KEY: peptide
LOCATION: (1)..(438)
OTHER INFORMATION: Ceres Seq. ID no. 12666051
NAME/KEY: peptide
LOCATION: (1)..(495)
                                       FEATURE
  ENGTH: 495
   Local
  Local Similarity
  410 WLLAAFT
   60 WALAAFS
   1 WMLSAFS
  1 WMLSAFS
  Similarity 5; Conserv
  Conservative
   Conservative
  416
   7
  76.3%;
57.1%;
   76.3%;
71.4%;
  Score 29;
Pred. No.
   Score 29; I
Pred. No. 2
  Mismatches
   Mismatches
  2.2e+02;
   DB 7;
  уь
2.5e+02;
1;
  DB 6;
  Length 495;
   Length 438;
   Indels
  Indels
   and
   Corresponding
   0;
  0
  Gaps
  0
   0
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  RESULT 39
US-11-056-355B-66754
   밁
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   ; OTHER INFORMATION: Ceres Seq. US-11-056-355B-66755
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                           Ş
   ; ORGANISM: Triticum aestivum 
US-10-953-349-31756
   US-10-953-349-31756
   RESULT 38
  US-11-056-355B-66754
  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 2750-1590PUS2 CURRENT APPLICATION NUMBER: US/11/056,355B CURRENT FILING DATE: 2005-02-14 PRIOR APPLICATION NUMBER: 60/544,190 PRIOR FILING DATE: 2004-02-13 NUMBER OF SEQ ID NOS: 119966 SEQ ID NO 66754 LENGTH: 530 TYPE: prt ORGANISM: Triticum aestivum
   CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31756
LENGTH: 530
   GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
  Sequence 66754, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
   Sequence 31756, Application US/10953349 Publication No. US20060107345A1
  Matches
   Query Match
Best Local
   Matches
   Best
  Query Match
   Query Match
   Matches
  FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(530)
OTHER INFORMATION: Ce
   APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
  Local Similarity
nes 5; Conserv
  Local Similarity
les 5; Conserv
   95 WALAAFS 101
   60 WALAAFS 66
 95
   1 WMLSAFS
  1 WMLSAFS 7
  Similarity
 WALAAFS 101
                                WMLSAFS 7
  Conservative
   Conservative
   Conservative
   7
  Ceres Seq.
  76.3%;
71.4%;
   76.3%;
71.4%;
   76.3%;
71.4%;
  Score 29; DB
Pred. No. 2.5e
1; Mismatches
   1;
  Score 29; DB 6; Pred. No. 2.7e+02; 1; Mismatches 1
  님
  IJ
  Score 29; DB 7;
Pred. No. 2.7e+02
   Mismatches
  no.
  по.
  14302422
  14302421
  DB 7; I
2.5e+02;
  1; Indels
  Length 530;
  Length 530
   Length 495;
   Indels
   0
  0
   0
  Gaps
   Gaps
   Gaps
  0
   0
   0,
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   RESULT 41
US-11-056-355B-82527
   밁
  RESULT 40
  ; OTHER INFORMATION: Ceres US-11-056-355B-82527
  US-11-056-355B-82523
   US-11-056-355B-82523
  Sequence 82527, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
   Sequence 82527, Application US/11056355B rublication No. US20060150283A1 GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav APPLICANT: Alexandrov, Nickolai
   NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 82527
   SEQ ID NO 82523
LENGTH: 564
  Matches
   Best
   Query Match
  Matches
   Query Match
  FILE REFERENCE: 2750-1590FUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
  CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 2750-1590PUS2
  NAME/KEY: peptide
LOCATION: (1)..(564)
OTHER INFORMATION: Ceres Seq. ID no. 12666046
  TYPE: prt
ORGANISM: Arabidopsis thaliana
FEATURE:
  TYPE: prt
ORGANISM: Arabidopsis thaliana
  FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(5
   LENGTH: 565
  Local Similarity nes 4; Conserv
   Local
   |:|:||:
536 WLLAAFT 542
537
  1 WMLSAFS 7
                                 1 WMLSAFS 7
  Similarity
4; Conserv
WLLAAFT 543
  Conservative
  Conservative
   (565)
   76.3%;
57.1%;
   76.3%;
57.1%;
  Seq. ID no. 12666050
  3; Mismatches
   Score 29; DB 7;
Pred. No. 2.9e+02;
   Score 29; DB 7;
Pred. No. 2.9e+02;
  Mismatches
   DB 7;
   Length 565;
   Length 564;
  Indels
  0
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  Gaps
  Gaps
  0
  0
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RESULT 42 US-10-449-902-47030 ; Sequence 47030, Application US/10449902 ; Publication No. US20060123505A1

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US-11-056-355B-66753
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   US-10-953-349-31755
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  RESULT 44
  RESULT 43
  US-10-449-902-47030
   US-10-953-349-31755
  APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILLE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 31755
LENGTH: 610
  Sequence 66753, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
   Sequence 31755, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
  Matches
   SEQ ID NO 47030
  Query Match
   Matches
  Query Match
   APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments
TITLE OF INVENTION: Folypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
  GENERAL INFORMATION:
   CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
   APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205YI-US
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
  SOFTWARE: PatentIn Ver. 2.1
  LENGTH: 599
TYPE: PRT
  ORGANISM: Triticum aestivum
   TYPE: PRT
  ORGANISM: Oryza sativa
   Local Similarity
les 5; Conserv
  Local
  175 WALAAFS 181
   168 WALAAFS 174
   1 WMLSAFS 7
  1 WMLSAFS 7
  Similarity 5; Conserv
   Conservative
   Conservative
  76.3%;
71.4%;
  76.3%;
71.4%;
  ; Score 29; DB
; Pred. No. 3.1e
1; Mismatches
   Score 29; DB 6;
Pred. No. 3e+02;
1; Mismatches
  DB 6; 1
3.1e+02;
  Length 599;
  Length 610;
   ٥,
   0;
   Gaps
   Gaps
   0
  0
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; ORGANISM: Zea mays subsp. mays US-10-953-349-33831
S
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  RESULT 45
US-10-953-349-33831
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   US-10-953-349-33830
   RESULT 46
US-10-953-349-33830
   US-11-056-355B-66753
   Sequence 33830, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT FILING DATE: 2004-09-30
CURRENT FILING
   Sequence 33831, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT FILING DATE: 2004-09-30
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
  SEQ ID NO 33830
LENGTH: 665
  SEQ ID NO 33831
  SEQ ID NO 66753
   Matches
   Matches
  Matches
   Query Match
   Query Match
  Best Local Similarity
Matches 5; Conserv
   Query Match
   TYPE: prt
ORGANISM: Triticum aestivum
FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(610)
OTHER INFORMATION: Ceres Seq. I
   ORGANISM: Zea mays subsp. mays
   LENGTH: 638
TYPE: PRT
   ENGTH:
   Local Similarity hes 5; Conserv
  Local Similarity
   175
   483
  1 WMLSAFS 7
  1 WMLSAF 6
      1 WMLSAF 6
  ហ
~:
   WALAAFS
   Conservative
  Conservative
   Conservative
   181
  76.3%;
83.3%;
  76.3%;
71.4%;
  76.3%;
83.3%;
  0
   0
  Score 29; DB 6;
Pred. No. 3.4e+02;
  Score 29; DB 6;
Pred. No. 3.2e+02;
  Score 29; DB 7; 1
Pred. No. 3.1e+02;
  ID no. 14302420
  Mismatches
   Mismatches
   Mismatches
   Length 638;
   Length 610;
   Length 665;
   Indels
   Indels
  0
   0
   0
   Gaps
   Gaps
  Gaps
  0,
   0
   0
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  S
  RESULT 49
US-11-056-355B-1495
  뭐
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   ; ORGANISM: Zea mays subsp. mays US-10-953-349-33829
  US-11-056-355B-1496
   US-11-056-355B-1496
   RESULT 48
  US-10-953-349-33829
   CURRENT APPLICATION NUMBER: US/10
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 33829
LENGTH: 667
  GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
  GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
  Sequence 33829, Application US/10953349 Publication No. US20060107345A1
  Sequence 1495, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
   NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 1496
   Sequence 1496, Application US/11056355B Publication No. US20060150283A1
   Matches
   Matches
   Query Match
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments
TITLE OF INVENTION: Polypeptides Encoded Thereby
  PRIOR APPLICATION NUMBER: 60/544,190 PRIOR FILING DATE: 2004-02-13
  CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
   NAME/KEY: peptide
LOCATION: (1)..(105)
OTHER INFORMATION: Ceres Seq.
  TYPE: prt
ORGANISM: Zea mays
FEATURE:
  TYPE: PRT
  LENGTH: 105
  Local
  Local Similarity
  100 WLLAAF 105
  512 WMLSRF 517
   1 WMLSAF 6
  1 WMLSAF 6
   Similarity 5; Conserv
   4.
   Conservative
   Conservative
  subsp.
  73.7%;
  76.3%;
83.3%;
   US/10/953,349
   Score 29; DB 6; Ler
Pred. No. 3.4e+02;
  Score 28; DB
Pred. No. 90;
   IJ
   Mismatches
   no.
   12411161
   DB 7;
   0;
   Length 667;
  Length 105;
   Indels
   Indels
                      and
   0,
   0
   Gaps
   0
   0
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; TYPE: prt
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(154)
; OTHER INFORMATION: Ceres Seq. II
US-11-056-355B-1494
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Search completed: August 29, Job time : 5.54455 secs
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   밁
   US-11-056-355B-1495
   US-11-056-355B-1494
   NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 1494
LENGTH: 154
  Sequence 1494, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
  SEQ ID NO 1495
LENGTH: 124
TYPE: prt
ORGANISM: Zea mays subsp. mays
  Matches
   Matches
   Best
   Query Match
  Query Match
   APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
  CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
  FILE REFERENCE: 2750-1590PUS2
   OTHER INFORMATION: Ceres Seq. ID no. 12411160
   NAME/KEY: peptide LOCATION: (1)..(1)
   FEATURE:
  Local
   Local
   119 WLLAAF
  149 WLLAAF 154
   l Similarity
4; Conserva
  l Similarity
4; Conserv
   1 WMLSAF 6
   1 WMLSAF
   Conservative
  Conservative
   (124)
   73.7%;
  73.7%;
                2006, 11:29:12
  Score 28; DB Pred. No. 1.1e 2; Mismatches
  ID no. 12411159
   Score 28; DB 7;
Pred. No. 1.3e+02;
   Mismatches
  DB 7;
  .1e+02;
   Length 154;
  Length 124;
   Indels
   ç.
  0
   0
  0
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